Stochastic optimization methods for extracting cosmological parameters from CMBR power spectra

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The reconstruction of the CMBR power spectrum from a map represents a major computational challenge to which much effort has been applied. However, once the power spectrum has been recovered there still remains the problem of extracting cosmological parameters from it. Doing this involves optimizing a complicated function in a many dimensional parameter space. Therefore efficient algorithms are necessary in order to make this feasible. We have tested several different types of algorithms and found that the technique known as simulated annealing is very effective for this purpose. It is shown that simulated annealing is able to extract the correct cosmological parameters from a set of simulated power spectra, but even with such fast optimization algorithms, a substantial computational effort is needed.

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I. INTRODUCTION

In the past few years it has been realized that the Cosmic Microwave Background Radiation (CMBR) holds information about virtually all relevant cosmological parameters [1,2]. The shape and amplitude of the fluctuations in the CMBR are strongly dependent on such parameters as \( \Omega, H_0 \) etc. [3]. Given a sufficiently accurate map of fluctuations it should therefore in principle be possible to extract information on the values of these parameters. In general, it is customary to describe the fluctuations in spherical harmonics

\[
\frac{\Delta T}{T}(\theta, \phi) = \sum_{lm} a_{lm} Y_{lm}(\theta, \phi),
\]

where the \( a_{lm} \) coefficients are related to the power spectrum by \( C_l = \langle a_{lm}^* a_{lm} \rangle_m \). For purely Gaussian fluctuations the power spectrum contains all statistical information about the fluctuations [3].

The CMBR fluctuations were first detected in 1992 by the COBE satellite [4], and at present the COBE measurements together with a number of smaller scale experiments [5] make up our experimental knowledge of the CMBR power spectrum. These data are not of sufficient accuracy to really pin down any of the cosmological parameters, but the next few years will hopefully see an explosion in the amount of experimental data. Two new satellite projects, the American MAP and the European PLANCK [6], are scheduled and are designed to measure the power spectrum precisely down to very small scales \((l \sim 1000 \text{ for MAP and } l \sim 2000 \text{ for PLANCK})\). This should yield sufficient information to determine almost all relevant cosmological parameters.

However, using CMBR data to extract information about the underlying cosmological parameters will rely heavily on our ability to handle very large amounts of data (Refs. [7,8,9] and references therein). The first problem lies in constructing a power spectrum from the much larger CMBR map. If there are \( m \) data points, then the power spectrum calculation involves inversion of \( m \times m \) matrices (an order \( m^3 \) operation). For the new satellite experiments \( m^3 \) is prohibitively large [7,8,9], and much effort has been devoted to finding methods for reducing this number by exploiting inherent symmetries in the CMBR [10]. However, once the power spectrum has been constructed the troubles are not over. Then the space of cosmological parameters has to be searched for the best-fit model. If there are \( n \) free cosmological parameters, each sampled by \( q \) points, then the computational time scales as \( q^n \) and, if \( n \) is large, the problem becomes intractable. In the present paper we assume that a power spectrum has been constructed, so that only the problem of searching out the cosmological parameter space remains.

In general, parameter extraction relies on the fact that for Gaussian errors it is possible to build a likelihood function from the set of measurements [10,11]:

\[
\mathcal{L}(\Theta) \propto \exp \left( -\frac{1}{2} x^T [C(\Theta)^{-1} x] \right),
\]

where \( \Theta = (\Omega, \Omega_b, H_0, n, \tau, \ldots) \) is a vector describing the given point in parameter space. \( x \) is a vector containing all the data points. This vector can represent either the CMBR map, or the reconstructed power spectrum points. \( C(\Theta) \) is the data covariance matrix.

Assuming that the data points are uncorrelated, so that the data covariance matrix is diagonal, this can be reduced to the simple expression, \( \mathcal{L} \propto e^{-\chi^2/2} \), where

\[
\chi^2 = \sum_{l=1}^{N_{\text{max}}} \frac{(C_{l,\text{obs}} - C_{l,\text{theory}})^2}{\sigma(C_l)^2},
\]

is a \( \chi^2 \)-statistics and \( N_{\text{max}} \) is the number of power spectrum data points [10].
In order to extract parameters from the power spectrum we need to minimize $\chi^2$ over the multidimensional parameter space.

In general there is no easy way of doing this. The topology of $\chi^2$ could be very complicated, with several different local minima. However, let us for now ignore this possible problem and assume that the function is unimodal. Then there exist a vast number of algorithms for extremizing the function. The most efficient methods work on completely general continuously differentiable functions, but under the right assumptions, $\chi^2$ possesses qualities which makes it possible to improve on the simple gradient methods. In general, the second derivative of $\chi^2$ with respect to parameters $i$ and $j$ is

$$
\frac{\partial^2 \chi^2}{\partial \theta_i \partial \theta_j} = 2 \sum_{k=2}^{N} \frac{1}{\sigma_k^2} \left[ \frac{\partial C_i}{\partial \theta_i} \frac{\partial C_i}{\partial \theta_j} - (C_{i,\text{obs}} - C_{i}) \frac{\partial^2 C_i}{\partial \theta_i \partial \theta_j} \right]
$$

(Sufficiently close to the minimum of $\chi^2$, the second term in the equation above should be small compared with the first. In practice this means that we get the second derivative information “for free” by just calculating the first derivative. Therefore, if we assume that the starting point for the optimization is sufficiently close to the true minimum, an algorithm utilising second-derivative information should converge much faster than a gradient method. The most popular algorithm of this type is the Levenberg-Marquardt method. Note, however, that far away from the minimum, the above expression for the second derivative can be very wrong and cause the algorithm to converge much slower.

Both gradient and second order algorithms are typically very efficient. However, there are several weaknesses: 1) They rely on our ability to calculate derivatives of $\chi^2$. Although in principle this is no problem, numerical experiments have shown that results for this derivative are not always reliable. For instance, the numerical code for calculating power spectra, CMBFAST, is fundamentally different for open and flat cosmologies, and has no implementation of closed models, so that the derivative of $\chi^2$ with respect to $\Omega_0$ is not reliable at $\Omega_0 = 1$. This is just one example, but the problem is generic as soon as points are located sufficiently near parameter boundaries. 2) The next problem is related to the fact that the above methods in general work as steepest descent methods. This means that they are very easily fooled into taking the shortest path towards some local minimum which needs not be global. If there are either many local minima or the topology of $\chi^2$ is complicated with many near degeneracies, then the above gradient-based methods are likely to perform poorly. Unfortunately this might easily be the case with any given realization of the CMBR power spectrum.

II. STOCHASTIC OPTIMIZATION

A. Multistart algorithms

The above caveats lead us to look for more robust methods for finding the true minimum of $\chi^2$. As soon as we are dealing with multimodal functions it is clear that we cannot contend ourselves with just running an optimization scheme based on the above method with just one starting point. The simplest possible improvement on the above method is a Monte Carlo multi start algorithm. In this case a starting point is chosen at random in the parameter space, and optimization is performed, using either a gradient or a second-order method. After the algorithm converges a new starting point is chosen. This method has the advantage that it converges to the global minimum in the asymptotic limit of infinite computational time. However, it is easy to improve on it, because the simple multistart algorithm will detect the same local minimum many times uncritically.

The multi level single linkage (MLSL) algorithm tries to alleviate this problem by mapping out the basins connected with the different local minima. If it detects that a trial point lies within a basin which has already been mapped, then the point is rejected. Depending on the type of objective function this algorithm can perform exceedingly well.

In what follows we use the simple implementation of the MLSL algorithm provided by Locatelli. First, we need the following definition: Let $x_{\max}$ and $x_{\min}$ be the maximum and minimum allowed value of parameter $i$. Then define a new parameter $q \equiv (x - x_{\min})(x_{\max} - x_{\min})$, so that $q \in [0, 1]$. We use this new parameter $q$ in the algorithm below, so that all cosmological parameters are treated on an equal footing and the allowed region is a simple hypercube spanning all values from 0 to 1 in $\mathbb{R}^n$. The algorithm is then devised as follow:

1) At each step, $k$, pick out $N$ sample points from the allowed region and calculate the objective function.
2) Sort the whole sample of $kN$ points in order of increasing $\chi^2$ value and select the $\gamma kN$ points with smallest values.
3) For all of these points, run optimization on given point $q$, if

- No point $y$ exists so that $d(q, y) < \alpha$ and $\chi^2(y) \leq \chi^2(q)$
- $d(q, S) > d$
- Optimization was not previously applied to $q$

Optimization is performed with a gradient method.
4) Proceed to step $k + 1$.

In the above, $d(q, y)$ is the Euclidean distance between $x$ and $y$, and $S$ is the set of already discovered local minima. $\alpha$ and $d$ are predefined distances which should be chosen to optimize the rate of finding local minima. They
are a measure of how large the basins connected with local minima are in general in that specific problem. The above method thus includes a host of different parameters which should be chosen by the user, \(N, d, \gamma\) and \(\alpha\). This can make it quite troublesome to devise an algorithm which performs optimally. In our implementation we have chosen \(N = 10, \gamma = 0.2, d = 0.1\) and \(\alpha = 0.1\). Note that this is somewhat in conflict with the definition given by Refs. [16,18], in that \(\alpha\) should really be a quantity which depends on \(k\), but in order to obtain a simple implementation we have used the above values.

## B. Simulated annealing

A completely different method, which in the next section is shown to be very effective for \(\chi^2\) minimization on CMBR power spectra, is simulated annealing.

The method of simulated annealing was first introduced by Kirkpatrick et al. in 1983 [19,20]. It is based on the behaviour of thermodynamic systems. Consider a thermodynamic system in contact with a heat bath at some temperature, \(T\). If left for sufficiently long the system will approach thermal equilibrium with that temperature. The heat bath is then cooled, and if this is done slowly enough the system maintains equilibrium in the cooling phase, and finally as \(T \to 0\) settles into the true ground state, the state with the lowest possible energy. This is very similar to global searches for minima of functions and simulated annealing relies on the fact that the function to be minimized can be considered as the energy of a thermodynamic system. If the system is then cooled from a very high “temperature” towards \(T = 0\) it should find the global minimum, given that it maintains thermal equilibrium at all times.

In practise one lets the system jump around in parameter space at random. Given a starting point \(i\), a trial point is sought according to some prescription, and is then either accepted or rejected according to the Metropolis acceptance probability [21]

\[
P_{\text{accept}}(i + 1) = \begin{cases} 
1 & \text{for } E_{i+1} \leq E_i \\
\frac{1}{e^{-(E_{i+1} - E_i)/T}} & \text{for } E_{i+1} > E_i 
\end{cases},
\]

where, in our case \(E = \chi^2\). There are very many similarities between this and thermodynamic systems, at high temperatures the system visits all states freely, while at low temperatures it can visit only states very close to the minimum. For instance it has been shown that by using the above criterion the system asymptotically approaches the Boltzmann distribution, given that it is kept at constant temperature asymptotically long [22]. Also, if a system undergoes simulated annealing with complete thermal equilibrium at all times then as \(T \to 0\) the energy approaches the global minimum [22]. For absolute global convergence to be ensured it is thus necessary to allow infinite time at each temperature.

In order to use simulated annealing for functional optimization it is necessary to specify three things:

1) A space of all possible system configurations
2) A cooling schedule for the system
3) A neighbourhood structure.

Here, the configuration space is a hypercube in \(R^n\) bounded by the limits on the individual parameters.

The cooling schedule and the neighbourhood structure are both something which in general are quite difficult to choose optimally [20]. Further, they make the scheme problem dependent. For this reason adaptive simulated annealing procedures have been devised which dynamically choose the cooling rate and neighbourhood directly from the previous iterations in order to maximize the thermalisation rate [23]. The problem with this approach is that the thermodynamic behaviour is no longer well-defined. For instance the approach to a Boltzmann distribution is not ensured.

In the present work we choose a relatively simple cooling schedule and neighbourhood structure, neither of which are adaptive. In practise we start with an initial temperature, \(T_0\), which is then lowered exponentially by the following criterion \(T_{i+1} = \alpha T_i\), where \(\alpha\) is some constant. When the temperature reaches a final value \(T_f\) the algorithm stops. In this way \(\alpha\) is a function of the total number of steps, \(N_s\), given as \(\alpha = (T_f/T_0)^{1/N_s}\).

The neighbourhood search is devised so that at high temperatures the system is prone to make large jumps whereas at lower temperatures it mostly searches the nearest-neighbour points. In our specific model the parameter space consists of a vector, \(x\), of \(n\) free parameters, bounded from below by the vector, \(x_{\min}\), and from above by \(x_{\max}\). Let iteration point \(i\) have the value \((x_\beta)_i\) for the parameter labelled \(\beta\). Then the value of this parameter at iteration \(i + 1\) has acceptance probability given as

\[
P([(x_\beta)_{i+1}] \propto e^{-[(x_\beta)_{i+1} - (x_\beta)_i]/T_{s,\beta}},
\]

where

\[
T_{s,\beta} = A_\beta [(x_\beta)_{\text{max}} - (x_\beta)_{\text{min}}]/(T/T_0)^{1/2},
\]

and \(A_\beta\) is some constant, chosen to yield a good convergence rate. The above probability is set to 0 if \((x_\beta)_{i+1}\) is outside the allowed interval for the given parameter. This criterion for picking out trial points has the desired quality that it makes large jumps at high temperature and progressively smaller jumps as the temperature is lowered. If the objective function depends strongly on \(\beta\), then \(A_\beta\) should be small, whereas if it is almost independent of \(\beta\), \(A_\beta\) should be large. It is well known that \(\chi^2\) is almost degenerate in the parameter \(\Omega_m h^2\). Therefore it is natural to choose \(A_{\Omega_m h^2}\) to be small. In our implementation we have chosen the following values for the control parameters: \(T_0 = 10^4, T_1 = 2, A_{\Omega_m h^2} = 1/32, A_\beta = 1/8\) for \(\beta \neq \Omega_m h^2\).
Note that the method of simulated annealing was first applied to simulated CMBR data by Knox [24], for a relatively small model with four free parameters.

III. NUMERICAL RESULTS

A. Performance of different algorithms

In order to test the relative efficiency of the different optimization schemes we have tried to run $\chi^2$ minimization on synthetic power spectra. All the power spectra in the present paper have been calculated by use of the publicly available CMBFAST package [15]. To make calculations not too cumbersome we have restricted the calculations to a six-dimensional parameter space, characterised by the vector $\Theta = (\Omega_m, \Omega_b, H_0, n_S, N_\nu, Q)$. The model is taken to have flat geometry so that $\Omega_{\Lambda} = 1 - \Omega_m$. We start from an assumed true model with $\Theta = (0.5, 0.05, 50, 1, 3, 30$ $\mu K)$, i.e. fairly close to the currently favoured $\Lambda$CDM model [25]. Table I shows the free parameters, as well as the allowed region for each. We further assume that all $C_l$'s up to $l = 1000$ can be measured without noise. That is, the errors are completely dominated by cosmic variance, with the error being equal to

$$\sigma(C_l) = \sqrt{\frac{2}{2l+1}} C_l.$$  

From underlying statistics we have produced a single realisation which we take to be the measured power spectrum.

Since we have $N = 999$ synthetic data points, all normally distributed, $\chi^2$ of the data set, relative to the true, underlying power spectrum should have a $\chi^2$ distribution with mean $N$, and standard error $\sqrt{2N}$, so that

$$\chi^2 = 999 \pm 45.$$  

The specific synthetic data set we use has $\chi^2 = 1090.98$, i.e., it is within about $2\sigma$ of the expected value. If the optimization routine is optimal, then for each optimization run

$$\chi^2_{\text{minimization}} \leq \chi^2_*.$$  

The average of several optimization runs should preferably yield a value which is somewhat below $\chi^2_*$. We therefore have a measure of whether or not the optimization has been successful.

We have tested four different optimization algorithms on a subset of the full six-dimensional parameter space. The algorithms are: Simple Monte Carlo multistart with: 1) gradient optimization method (G), 2) Levenberg-Marquardt method (LM), 3) multi level single linkage (MLSL), as described in Section IIa, 4) simulated annealing, as described in Section IIb. Algorithms 1-3 use optimization routines from the PORT3 library [26].

![Graph showing the average $\chi^2$ found by different algorithms](image)

**FIG. 1.** The average $\chi^2$ found by the different algorithms. The data points are for 1) simple gradient method (triangles), 2) Levenberg-Marquardt method (squares), 3) multi level single linkage (crosses), and simulated annealing (diamonds). The top panel shows optimization for the case of four free parameters, whereas the bottom panel shows it for five parameters.

In order to make direct comparison between the algorithms, we have let them run for a fixed number of steps, where one step is defined equal to one power spectrum calculation. All methods, except simulated annealing, use gradient information, which means that additional power spectra must be calculated at each iteration. We use two sided derivatives, so that to calculate the gradi-
ent (and Hessian), we need $2n$ more calculations, where $n$ is the number of cosmological parameters. Fig. 1 shows the minimum $\chi^2$ found by the different algorithms. Each point in Fig. 1 stems from a Monte Carlo run of 15 optimizations.

Clearly, the MLSL method improves on the simple multi start algorithm. The LM algorithm performs better than gradient optimization in some cases, but in other cases it is much worse. This is probably due to the fact that if the starting point is far away from a local minimum then the second derivative may yield false information because Eq. (4) does not hold, causing the algorithm to converge slower. This weakness could be remedied to some extent by diagonalising the matrix of second-derivatives (Fisher matrix diagonalisation), so that the correlation between different parameters is approximately broken.

However, the most striking feature in Fig. 1 is that SA outperforms the other algorithms easily. Most likely this is due to the fact that $\chi^2$ possesses valleys where the function has many almost degenerate local minima. Note that the likelihood function does not need to be truly multi-modal for this effect to occur. It can happen either because the parameter space is constrained so that the algorithm takes a path which leads out of the allowed space, or because there are small “bumps” on $\chi^2$ close to the global minimum, which cause the gradient algorithms to get trapped. $\chi^2$ is not multimodal in the sense that it contains equally good local minima, separated by long distances in parameter space.

In Fig. 2 we show four different runs of the simple gradient-based algorithm without multi-start. In two of the cases the algorithm converges towards the global minimum, whereas in the two other it becomes trapped at much higher lying points in parameter space. We have tested the effect of varying step size in the gradient calculation and found that the results do not depend on this. This figure also shows that the gradient based algorithms generally converge fairly rapidly (i.e. a few hundred steps), so that the multi-start algorithm generally runs several times even for relatively a relatively small number of total steps.

### B. Parameter extraction

If the $\chi^2$ minimization succeeds in finding the global minimum, then the value found should reflect the underlying measurement uncertainty. We have performed a detailed Monte Carlo study of how well the SA algorithm is able to extract parameters from the power spectrum. The test goes as follows: First, construct $N_{MC}$ synthetic measured power spectra, as described in the previous section. Then run optimization on each one of these spectra. This produces $N_{MC}$ estimated points in parameter space. In order to compare these points with the underlying uncertainty, we then need to calculate the estimated standard error on the different parameters. This is done by the standard method of calculating the Fisher information matrix. At the true point in parameter space, the likelihood function should be maximal, so that it should have zero gradient. The matrix of second derivatives is then given by (Eq. (10))

$$I_{ij} = \sum_{l=2}^{l_{\text{max}}} (2l + 1)C_l^{-2} \frac{\partial C_l}{\partial \theta_i} \frac{\partial C_l}{\partial \theta_j}, \quad \text{(11)}$$

The expected error on the estimation of parameter $i$ is then given by

$$\sigma_i^2 \simeq (I^{-1})_{ii}, \quad \text{(12)}$$

if we assume that all the relevant cosmological parameters should be determined simultaneously. The expected error on $\Omega_m$ is $\sigma = 0.098$, given our assumed measurement precision. Note that above we have again assumed that the only uncertainty in the measurements is from cosmic variance.

We have performed this Monte Carlo test on the 6-dimensional parameter space, using 24 different synthetic spectra. We have extracted parameters using SA with a different number of total steps: 500, 2000 and 4000. Fig. 3 shows how the estimated points are distributed for the parameter $\Omega_m$. We have binned the extracted points in bins of width $1\sigma$ up to $5\sigma$. For the optimization performed with 500 steps the distribution is very wide, showing no specific centering on the true parameter value. The optimization with 2000 steps extracts

![FIG. 2. Four different runs of the simple gradient method (G), without multi-start.](image)
values which are centered on the true value, indicative of a good optimization. Furthermore, the optimization with 4000 steps shows little improvement over that with 2000, again indicating that the one with 2000 steps is already performing optimally. Note that both for 2000 and 4000 steps the distribution of extracted points is significantly wider than the theoretical expectation which was calculated assuming a normal distribution with \( \sigma = 0.098 \). One would expect this to be the case since the probability distribution of any given parameter is only normal close to the true value, even for a perfect optimization. Therefore there are likely to be more outlying points than suggested by the normal distribution.

\[
\chi^2_\theta = \sum_{i=1}^{N_{MC}} \frac{1}{\sigma^2} (\theta_{\text{found}} - \theta_{\text{true}})^2.
\]

This function should be approximately \( \chi^2 \) distributed. We have calculated \( \mu \) and \( \chi^2 \) for the sample of extracted parameters, to see if it is compatible with the theoretical expectations. Table II shows the values found from the 24 Monte Carlo simulations. The sample mean found by the optimization with 500 steps deviates by more than \( 7\sigma \) from the expectation. Again this indicates a poor optimization. The optimizations with 2000 and 4000 steps succeed in recovering the true mean to within \( 2\sigma \). As for \( \chi^2 \), it is much lower for the 2000 and 4000 steps optimizations than for the 500 steps. However, both are still much larger than expected from a normal distribution. As mentioned above this has to do with the fact that the distribution is not normal far away from the true parameter value, so that more outlier points are expected. These contribute heavily to \( \chi^2 \), so that a larger value can be expected, even for a perfect optimization.

As seen above, even for the small 6 parameter model we use, it is necessary on average to calculate more than \( 10^3 \) power spectra. Even on a fast computer this is something which takes several hours. This must be done each time one wants to check how a new proposed cosmological model fits the data. This very clearly shows the necessity of using fast optimization algorithms for parameter extraction.

Note that the models we have calculated are flat and without reionization, including either curvature or reionization significantly slows the CMBFAST [15] code. Also, more exotic models like scenarios with decaying neutrinos lead to very cumbersome CMBR spectrum calculations [27].

The above Monte Carlo method was also used by Knox [24] in order to test the \( \chi^2 \) optimization efficiency for a small model with 4 free parameters.

![Diagram](image)

**FIG. 3.** Values of \( \Omega_m \) found by the optimization procedure for the 24 Monte Carlo runs. The recovered values are shown in bins of width 1\( \sigma \), where \( \sigma = 0.098 \) and \( \Delta \theta = |\Omega_m,\text{found} - 0.5| \). The full line is the theoretical expectation, assuming that errors on \( \Omega_m \) are normally distributed.

If we have \( N_{MC} \) Monte Carlo runs, then if the optimization is perfect one should obtain a sample mean of roughly

\[
\mu_{\text{sample}} \simeq \mu_{\text{true}} \pm \sigma_s,
\]

where \( \sigma_s = \sigma/\sqrt{N_{MC}} \) for a given parameter if \( N_{MC} \) is large and the extracted parameters are drawn from a normal distribution. We can also calculate \( \chi^2 \) for the sample

\[
\chi^2_\theta = \sum_{i=1}^{N_{MC}} \frac{1}{\sigma^2} (\theta_{\text{found}} - \theta_{\text{true}})^2.
\]

**TABLE II.** Recovered mean value and \( \chi^2 \) for the 50 Monte Carlo runs performed, for the parameter \( \Omega_m \). Values in parentheses are the expected theoretical values.

| Steps | \( \Omega_m \) | \( \mu_{\text{sample}} \) | \( \chi^2 \) |
|-------|----------------|----------------|-------------|
| 500   | 0.665 (0.50 ± 0.020) | 198.4 (50 ± 10) |
| 2000  | 0.499 (0.50 ± 0.020) | 73.7 (24 ± 6.9) |
| 4000  | 0.474 (0.50 ± 0.020) | 67.7 (24 ± 6.9) |
IV. DISCUSSION AND CONCLUSIONS

We have tested different methods for $\chi^2$ minimization and parameter extraction on CMBR power spectra. It was found that simulated annealing is very effective in this regard, and that it compared very favourably with other optimization routines. The reason for this is most likely that $\chi^2$ possesses very nearly degenerate minima. Also, numerical noise in the CMBFAST code can cause the gradient information to become unreliable near stationary points, causing the gradient based methods to become trapped in points which are not true minima.

We have also found that even for the simulated annealing algorithm, many power spectrum calculations are usually necessary in order to obtain a good estimate of the global minimum. Without a fast optimization algorithm it is difficult to extract reliable parameter estimates from CMBR power spectra, and even with a routine like SA, it is computationally very demanding as soon as the parameter space is realistically large (9-10 dimensional).

Note that all of the above calculations rely on stochastic methods in that they start out at completely random points in the allowed parameter space. This is very different from the method used by Oh, Spergel and Hinshaw [9], who use as the initial point a fit obtained by the chi-by-eye method and then optimize that initial guess using a second order method. This method surely makes the optimization algorithm converge faster, but suffers greatly from the problem of how to choose the initial point without biasing the outcome (i.e. making the algorithm find a minimum which is not global). We believe that using stochastic optimization is a much more robust way of optimization.

Interestingly, there are other modern algorithms for optimization which work along some of the same principles as SA, for instance genetic algorithms [28]. Given the magnitude of the computational challenge provided by upcoming CMBR data, it appears worthwhile to explore the potential of such new algorithms.

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