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ESTIMATION OF INTEREST
RATE TERM STRUCTURE**

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Abstract

The term structure of interest rates is an instrument that gives us the necessary information for valuing deterministic financial cash flows, measuring the economic market expectations and testing the effectiveness of monetary policy decisions. However, it is not directly observable and needs to be measured by smoothing data obtained from asset prices through statistical techniques. Adjusting parsimonious functional forms – as proposed by Nelson and Siegel (1987) and Svensson (1994) – is the most popular technique. This method is based on bond yields to maturity and the high degree of non-linearity of the functions to be optimised make it very sensitive to the initial values employed. In this context, this paper proposes the use of genetic algorithms to find these values and reduce the risk of false convergence, showing that stable time series parameters are obtained without the need to impose any kind of restrictions.

Keywords: forward and spot interest rates; Nelson and Siegel model; non-linear optimization; numerical methods; Svensson model; yield curve estimation.

JEL classification: G12, C51, C63

1 Introduction

The term structure of interest rates is defined as the relationship between the basic nominal interest rates in an economy and the time to maturity of the default free cash-flows whose prices are used to obtain them.¹ It is a very useful tool, not only in finance, where it is used to value financial assets, manage financial risks and make portfolio and corporate finance decisions; but also in macroeconomic analysis and in the implementation and evaluation of monetary policy, where it is widely used.

This functional relationship has two basic characteristics due to the usual no-arbitrage hypothesis: continuity and smoothness. Having smoothness guarantees the continuity of the implicit term structures of forward interest rates, which is also required in a no-arbitrage financial context. The absence of government zero-coupon bonds with maturity at all of the terms of the structure determines its unobservability. Thus, we need to obtain this structure through: the few spot interest rates directly observed by the price of zero-coupon government bonds; and the price of government coupon bonds, which can be seen as a portfolio of zero-coupon bonds, from both the theoretical and the practical point of view,² and allow us to cover the entire temporal spectrum of the term structure of interest rates.

This need has promoted a vast line of research focussing on obtaining the best representation of the underlying term structure in the market price of government bonds. From the beginnings of this research in 1929 until now, we have gone from the use of graphic, subjective and handmade methods [Anderson et al. (1996)], to the use of sophisticated non-parametric methods that fit spline functions gradually smoothed with respect to terms [Anderson and Sleath (2001)].

In this context, the simple functional forms that describe the whole temporal spectrum of the structure of interest rates, parsimonious in parameters and easy to implement, have been and are the most widely used by central banks in their estimations. To be more precise, the function developed by Nelson and Siegel (1987) and its augmented version, proposed by Svensson (1994) (hereafter the NSS functions) are currently used by nine of the thirteen central banks that inform the Bank for International Settlements of their estimations [BIS (2005)].³ Hence the special relevance of studies such as this, which are directed towards achieving better use of these models in practice.

The choice of these simpler techniques is wholly justified when their use is restricted to the analysis of investments and monetary policy.⁴ Despite this, from the estimations made in parallel by the Riksbank, Dillén and Peterson (2005) infer that “the quantitative difference between the augmented Nelson and Siegel method and the smoothed splines approach is normally very small”. Moreover, the estimated parameters of these simple polynomial

1. Here, we are referring to spot interest rates although the term structure of interest rates can also be defined with reference to par yields, to implicit forward interest rates or to associated discount factors; all of which are variables related directly with spot interest rates.

2. Strips, segregated cash flows of bonds with periodic coupon payments, are instruments traded on secondary markets similar to zero-coupon bonds and therefore spot interest rates can be directly taken from them, although the influence on their quote of spreads related to market microstructure should be considered.

3. In the financial literature there are other proposals of simple functional forms although they are less used. Chief among them are those of McCulloch (1971), Chambers et al. (1984), Diament (1983) and Mansi and Philips (2001).

4. Other uses of the term structure of interest rates, such as those related to no-arbitrage valuation and the valuation of fixed-income assets and derivatives, need more accurate estimations of the term structure.

functions have been used in financial pricing developments, i.e. modelling government bond yields, either directly [Diebold and Li (2005); Diebold, Ji and Li (2005)], or adding macroeconomic factors [Diebold, Rudebusch and Aruoba (2005); Diebold, Piazzesi and Rudebusch (2005)].

One of the most important technique questions in the day-to-day fitting process of the NSS functions is, undoubtedly, the risk of achieving parameters corresponding to a local optimum and not to the global optimum relative to the data, i.e., the risk of false convergence.⁵ This risk comes from the high level of non-linearity of the functions to be fitted and in practice is often detected by the poor fit with regard to conventional levels, i.e., a posteriori.

This problem is clearly shown by the high sensitivity of the estimated parameters, and not necessarily of goodness-of-fit, to the initial values used in the implementation of the usual nonlinear optimization algorithms, i.e. maximum likelihood and nonlinear least squares.⁶ This situation brings about a significant empirical consequence: namely, when the initial parameters are fixed, regardless of the procedure followed for their determination, the estimated parameters experience great variability.

The objective of this paper is to develop an estimation procedure for these functions that avoids the problem generated by the choice of the initial values in the optimization process as it always entails some degree of discretion.⁷ To this end, we propose the use of genetic algorithms in the fitting process of the NSS functions to the term structure of the interest rates, thus obtaining more than satisfactory results because, besides giving a solution to the false convergence risk, the use of genetic algorithms generates series of parameters with less volatility and a more accurate fit to the underlying term structure of the interest rates.

The rest of this paper is structured as follows. Section 2 describes the NSS functions. Section 3 shows and analyses the estimations of the term structure in the Spanish government bond market through the traditional optimization methods. Section 4 reports the results of re-estimating the term structures, this time using genetic algorithms, and compares them with those of Section 3. Finally, Section 5 concludes.

5. In the estimation of the term structure other problems appear that are not considered here, although not because they are thought to be irrelevant. The most important are: deciding on the variable whose errors must be minimized in the fit process; choosing bonds with adequate liquidity; and determining the influence of taxes on the prices used.

6. In this context, Maximum likelihood method assumes that differences between observed and theoretical yields are normally distributed, becoming, in fact, equivalent to an estimation based on least squared error of yields. Among the countries that report their estimations to the BIS and use NSS functions, Switzerland, Finland and Norway fit for maximum likelihood, whereas Italy and Spain use nonlinear least squares.

7. For example, the central bank of France uses constant initial coefficients derived in a heuristic form in order to minimize the number of non-convergence points between 1992 and 1994.

2 The Nelson–Siegel–Svensson functions

Nelson and Siegel (1987) propose a parametric model, in which the instantaneous forward rates at t have a functional form corresponding to the following exponential expansion,

$$f_t(m) = \beta_{t,0} + \beta_{t,1} \exp\left(\frac{-m}{\tau_t}\right) + \beta_{t,2} \frac{m}{\tau_t} \exp\left(\frac{-m}{\tau_t}\right) \quad (1)$$

where m is the term, and β_0 , β_1 , β_2 and τ are the parameters to be estimated.

This function, $f(m)$, has convenient and desirable characteristics to capture the term structure shape. One of them is the existence of the limit of function $f(m)$ for $m=\infty$ and for $m=0$, i.e.:

$$\begin{aligned} \lim_{m \rightarrow \infty} f(m) &= \beta_0 \\ \lim_{m \rightarrow 0} f(m) &= \beta_0 + \beta_1 \end{aligned} \quad (2)$$

which allows the computation of both very long and very short-term instantaneous forward interest rates.

The way in which the transition is produced between the very short-term rate and the very long-term rate is captured by parameters β_2 and τ , so that if β_2 is negative the curve would form a “U” shape, whereas if it is positive, it would form an inverted “U” shape, and if β_2 is close to zero, as opposed to a maximum or minimum, we have a sigmoid shaped function. The speed at which the forward interest rate approaches its very long-term value is defined by τ^{-1} .

The spot interest rates derived from the Nelson-Siegel model for the instantaneous forward interest rates are obtained by integrating expression (1) in the expression that relates the spot and forward interest rates:

$$s_t(m) = \frac{1}{m} \int_0^m f_t(u) d(u) \quad (3)$$

obtaining:

$$s_t(m) = \beta_{t,0} + \left(\beta_{t,1} + \beta_{t,2}\right) \left(\frac{\tau_t}{m}\right) \left(1 - \exp\left(\frac{-m}{\tau_t}\right)\right) - \beta_{t,2} \exp\left(\frac{-m}{\tau_t}\right) \quad (4)$$

in which, as with the instantaneous forward interest rates function, the parameters have the following interpretation: β_0 is the very long-term interest rate, $\beta_0 + \beta_1$ is the short-end value of the curve, while β_2 and τ , determine the way in which the transition is produced between this short-end value and the asymptote in the very long-term.

For this function to make economic sense, insofar as spot interest rates due to their nominal character are by definition strictly positive, the parameters are restricted by the following conditions:

$$\begin{aligned}\beta_0 &> 0 \\ \beta_0 + \beta_1 &> 0 \\ \tau &> 0\end{aligned}\tag{5}$$

In this way, we ensure through the first two inequations that the two extremes of the curve are positive, whereas the third inequation ensures that the function is asymptotic in the very long-term.

Svensson (1994) enlarges the Nelson and Siegel model (1987) in order to allow for a second hump or depression, through adding another term to equation (1) of the instantaneous forward rate

$$f_t(m) = \beta_{t,0} + \beta_{t,1} \exp\left(\frac{-m}{\tau_{t,1}}\right) + \beta_{t,2} \frac{m}{\tau_{t,1}} \exp\left(\frac{-m}{\tau_{t,1}}\right) + \beta_{t,3} \frac{m}{\tau_{t,2}} \exp\left(\frac{-m}{\tau_{t,2}}\right)\tag{6}$$

where the new parameters β_3 and τ_2 determine its greater flexibility.

The meaning and interpretation of these parameters is the same as with β_2 and τ_1 , so that a positive (negative) value for β_3 implies an additional “U” (inverted “U”) in the function. The position of this hump is determined by τ_2 , so that if $\tau_2 > \tau_1$ ($\tau_2 < \tau_1$) the effect of the last term disappears faster (slower), meaning that it will be before (after) the shape induced by β_2 and τ_1 . This function nests the Nelson-Siegel proposal, i.e., when $\beta_3 = 0$ or $\tau_1 = \tau_2$ the Svensson function becomes the Nelson-Siegel function.

As before, we can obtain an expression of the spot interest rates in t through the integration of the expression of the instantaneous forward interest rates, obtaining:

$$\begin{aligned}s_t(m) &= \beta_{t,0} + (\beta_{t,1} + \beta_{t,2}) \left(\frac{\tau_{t,1}}{m}\right) \left(1 - \exp\left(\frac{-m}{\tau_{t,1}}\right)\right) - \beta_{t,2} \exp\left(\frac{-m}{\tau_{t,1}}\right) + \\ &+ \beta_{t,3} \left(\frac{\tau_{t,2}}{m}\right) \left(1 - \exp\left(\frac{-m}{\tau_{t,2}}\right)\right) - \beta_{t,3} \exp\left(\frac{-m}{\tau_{t,2}}\right)\end{aligned}\tag{7}$$

Now, in order to make economic sense, the conditions on the function are:

$$\begin{aligned}\beta_0 &> 0 \\ \beta_0 + \beta_1 &> 0 \\ \tau_1 &> 0 \\ \tau_2 &> 0\end{aligned}\tag{8}$$

where, again, the first two conditions ensure that the rates at the extremes of the function are positive, while the final two allow for a finite limit at the long-end of the curve.

3 Traditional estimation of the Nelson–Siegel–Svensson functions

Figures 1-3 show the joint daily values of the estimated parameters in the Spanish market of the functional form proposed by Svensson (1994) for the period from January 1995 to February 2005. These estimations have been done through a traditional nonlinear optimization procedure, more precisely, through non-linear least squares. The variable selected to minimize the square of errors is the bond price weighted by the inverse of the square root of its duration.⁸ The price of the government bonds, selected to avoid liquidity problems, is calculated as the average of the bid and ask prices in the market at a fixed time on each trading day.⁹

An initial look at these parameters reveals the strong volatility in a large part of the series (especially in β_0 , β_1 , τ_1 and τ_2); the abundance of anomalous values (in the same parameters); and the frequency of structural changes in the series (mainly in parameters β_2 and β_3). This behaviour is not easily justifiable with the observed evolution of the Spanish economy in general and the Spanish government debt market in particular, and even less so if we compare the behaviour of each parameter with its particular economic meaning.

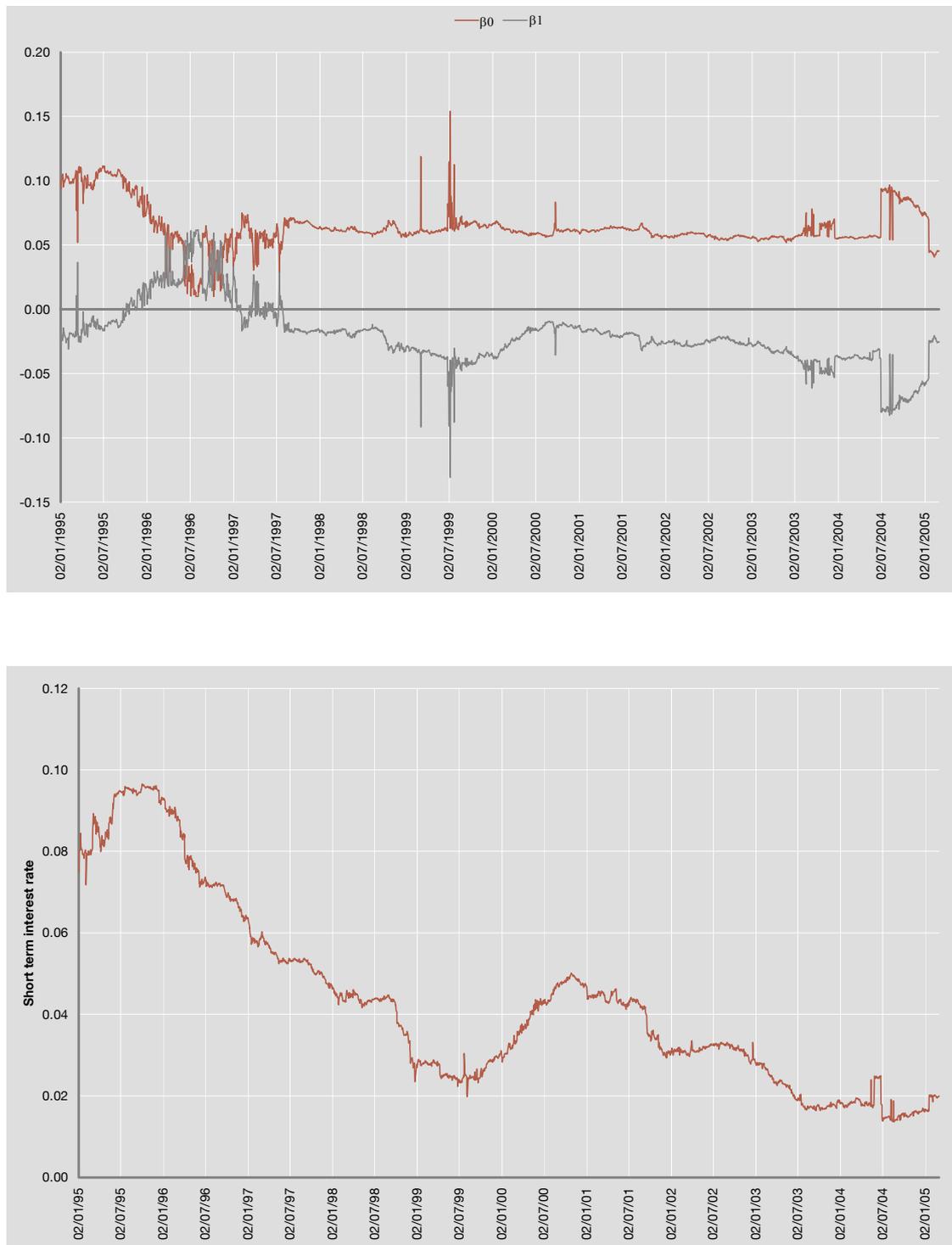
As Bolder and Strélski (1999) show, the estimation of the interest rate curve is very unstable and the need to optimize a nonlinear function makes it very sensitive to the initial values assigned to the parameters to be estimated. For a more in depth analysis of the behaviour of the series we need to make a more detailed study of the parameters' behaviour taking into account what they represent.

With regard to parameter β_0 , between 1995 and the end of 1997 figure 1 shows a period of strong volatility accompanied by a fall from an initial starting point of around 10% to below 2% at certain moments in this period, finally stabilizing slightly above 6%. This initial phase is followed by a long stage of stability at around 6% until the middle of 2004. This stability is interspersed with moments in which it experiences sharp rises which at times take it close to 12% and even to 15%. Between the middle and the end of 2004, we see how once again it returns to around 10%, only to fall rapidly at the beginning of 2005 to around 4%.

8. This criterion is followed by the central banks of Belgium, Canada, Finland, France, Italy, Spain and the United States.

9. We use a sample that includes daily prices of repos and zero-coupon bonds (terms of 1 day, 1 week, 2 weeks, 1 month, 3 months, 6 months and 1 year), as well as coupon bonds with more than a year to maturity.

Figure 1. Temporal evolution of the parameter estimators β_0 (long-term interest rate) and β_1 (top graph) and of short-term interest rates obtained as the sum of the two (bottom graph) from 2/01/1995 to 1/03/2005 measured through the estimation of the Svensson (1994) function obtained with the traditional optimization method.



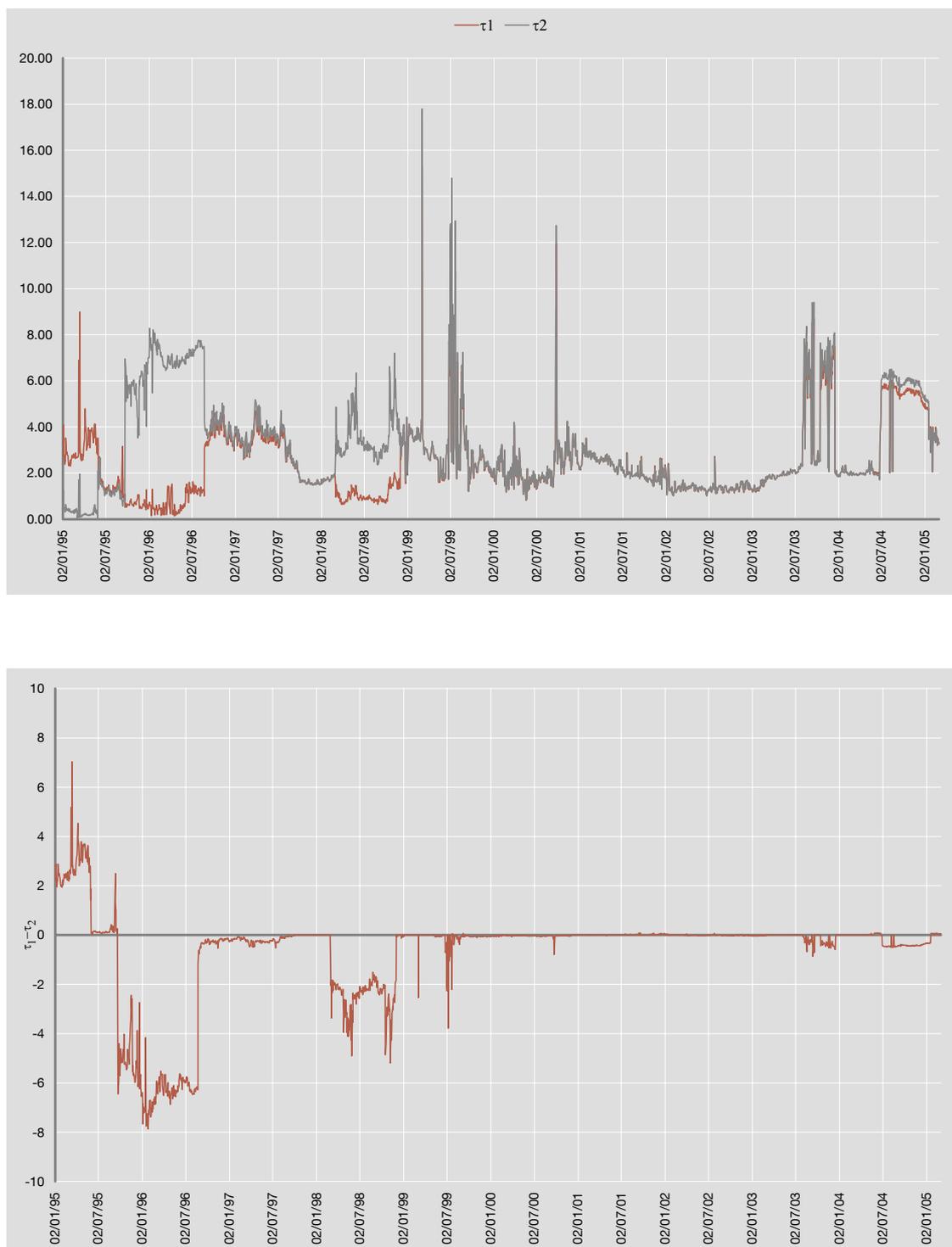
As we indicate in the previous section, β_0 represents the very long-term interest rate in the NSS framework. In this sense, although the uncertainty over the entry of Spain in the euro area may cause the strong volatility at the beginning of its series, and that this volatility may be replaced by stability as a result of the later growing credibility, neither the sudden changes in long-term interest rates in the later years nor values such as the 15% (6 July 1999) or the 12% (4 March 1999) are plausible.

Recall that the sum of parameters β_0 and β_1 captures the behaviour of the very short-term interest rate in the NSS framework. According to this, β_1 captures the differential between the very short and very long-term rates, implying an increasing temporal structure when it is positive and a decreasing slope in the interest rate curve when it takes a negative value. Figure 1 shows the behaviour of the estimator of β_0 and β_1 in the same period. We observe that the estimators of parameters β_0 and β_1 are most unstable in the following periods: between January 1995 and August 1997, where the volatility of the individual parameters is far higher than the volatility of the rest of the series; in July 1999, when there is a new episode of strong volatility in the series; and to a lesser extent, between 15 August and 15 December of 2003. We also see isolated sharp rises such as on 4 March 1999 and 22 September 2000. Finally, between 2 July 2004 and 18 January 2005 we see a truncated step.

It is particularly important to note that their behaviour reflects very similar movements but with the opposite sign. In fact, if we superpose the series of both parameters, as in figure 1, we can observe that jumps and anomalous values in the two series are extremely coincident in time, although with contrary signs, i.e., we observe symmetric behaviour. This behaviour is either the cause or the consequence of the fact that a large part of the volatility and the anomalous values found in the individual series disappears when their sum is considered. This fact shows that the estimation reached for the very short-term interest rate in the NSS framework is much more stable and of better quality than the estimation of the very long-term, and also that it is much closer to the real evolution of interest rates in this period.

When we jointly analyse parameters τ_1 and τ_2 , which are associated with the exponential functions and capture the speed of transition between the short and long-term rates (τ_1) and distortions in the curve (τ_2) in the NSS framework, as in figure 2, we see how, superposing the evolution of the series again, their values are extremely similar for the major part of the sample period. In fact, if we calculate the difference between the two estimators, as in figure 2, we find that it rarely moves away from zero.

Figure 2. Temporal evolution of the parameter estimators, τ_1 and τ_2 in the top graph and the difference between the two estimators ($\tau_1 - \tau_2$) in the bottom graph, from 2/01/1995 to 1/03/2005 measured through the estimation of the Svensson (1994) function obtained with the traditional optimization method.



The existence or not of significant differences between these two parameters is especially relevant, because if we could assume that $\tau_1 = \tau_2$, the two final terms of equation 6 could be grouped together and the Svensson model rewritten as follows,

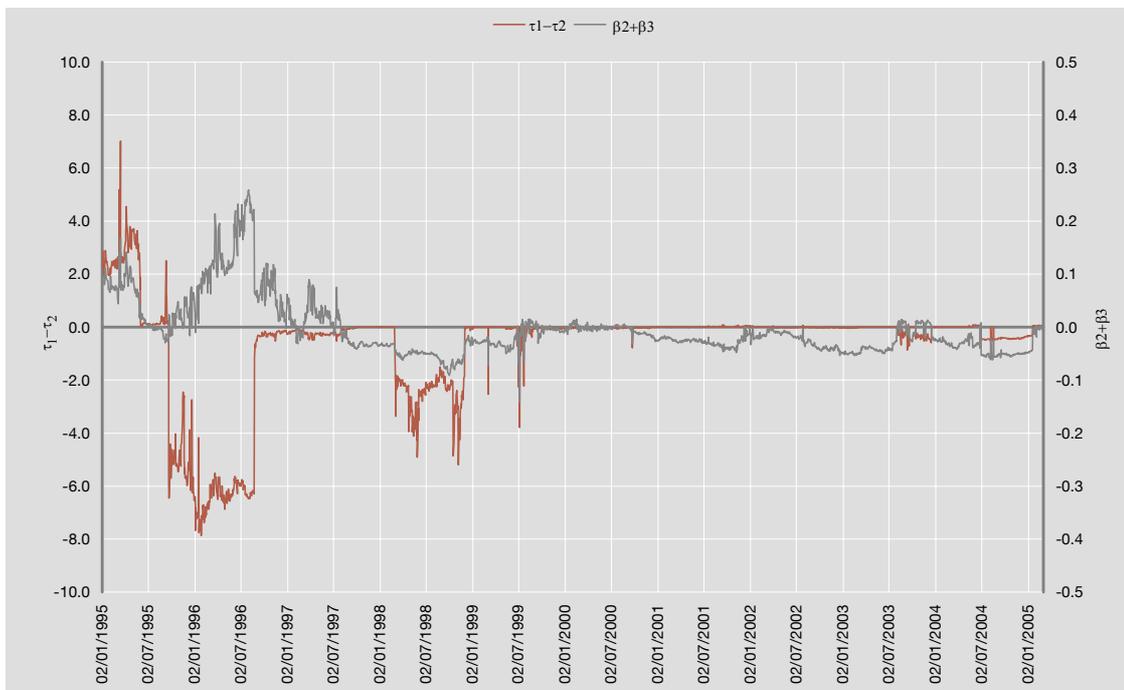
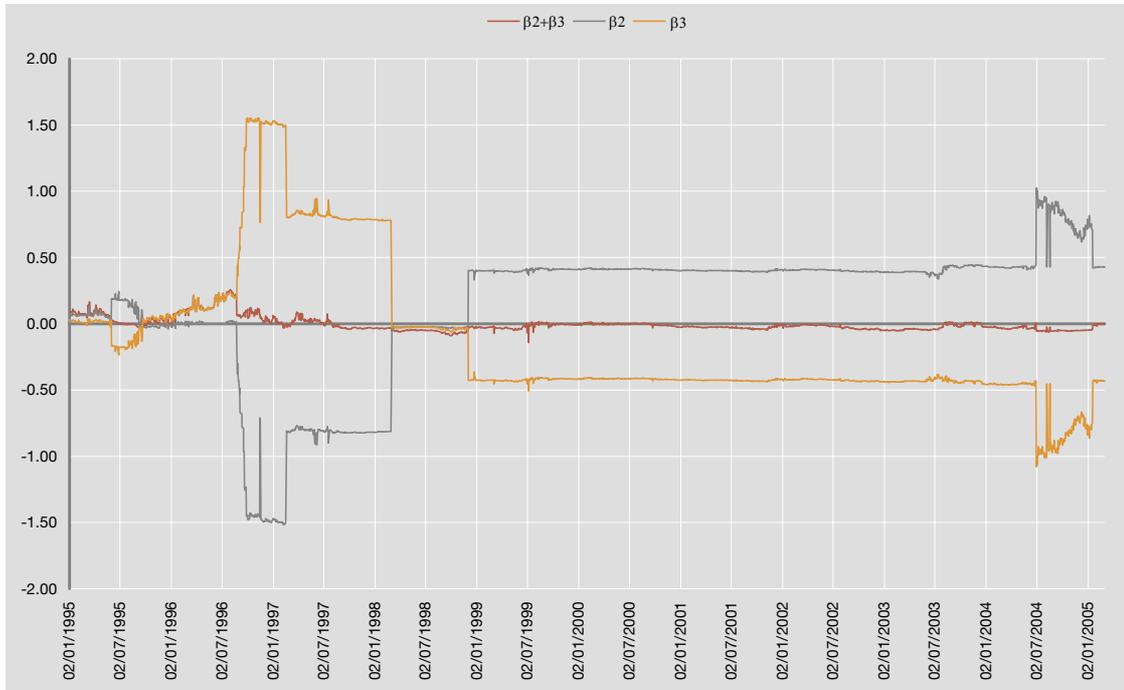
$$f_t(m) = \beta_{t,0} + \beta_{t,1} \exp\left(\frac{-m}{\tau_t}\right) + (\beta_{t,2} + \beta_{t,3}) \frac{m}{\tau_t} \exp\left(\frac{-m}{\tau_t}\right) \quad (9)$$

obtaining an identical expression to that of the model of equation (1) proposed by Nelson and Siegel (1987) which, by estimating only four parameters instead of six, is also more stable in its estimation.

If we analyse in which periods there are differences between the values of the two parameters, we find that: from 2 January of 1995 to 22 August 1996, we see clearly differentiated values in the two parameters, although there are two different parts, until 21 of September 1995, τ_1 is higher than τ_2 , whereas after this date the relationship is inverted; from 2 March 1998 to 30 November 1998 there is a new period of divergence between the two parameters; in July 1999 there is a new period with differentiated parameters, coinciding with a phase of high volatility in the very long-term interest rate estimations; between 15 August and 15 December 2003, again in concordance with rises in the series of long-term rates; and between 2 July 2004 and 18 January 2005. Additionally, we observe anomalous values on 4 March 1999 and 22 September 2000, as with β_0 and β_1 . Overall it seems that the sharp movements in the estimators of these parameters coincide temporally with the changes we have found in the characteristics of the estimations of very long-term interest rates.

Finally, figure 3 shows that the estimators of β_2 and β_3 follow an opposite behaviour, when one of them is positive, the other one is negative. Adding this to equation 9 that holds when τ_1 and τ_2 exhibits similar values, we can conclude that humps and “U” shapes terms plays a moderate role in the determination of the whole term structure.

Figure 3. Temporal evolution of the parameter estimators β_2 and β_3 and of the difference between the two (top graph) and of the differences between the parameters of speed ($\tau_1 - \tau_2$) and the sum of intensities ($\beta_2 + \beta_3$) (bottom graph) from 2/01/1995 to 1/03/2005 measured through the estimation of the Svensson (1994) function obtained with the traditional optimization method.



4 Estimation of the Nelson–Siegel–Svensson functions with genetic algorithms

Genetic algorithms (GA) were introduced by Holland (1975), and although there is no globally accepted definition of them, in the context of this paper they can be defined as stochastic algorithms for computationally intensive numerical optimization. Mitchell (1998) points out that GA must always have three characteristics: *selection*, *cross-over* and *mutation*. These can be made more definite in different ways in order to adapt to the particular problem analyzed.

4.1 Creation

In the model parameters estimation context, the possible model solution candidates can be considered as the *chromosomes* of a specific individual. In this sense, we have to randomly generate as many individuals as we consider necessary (N).¹⁰

In our particular case, each curve starts from a set of parameters (4 in the Nelson-Siegel and 6 in the Svensson) which will be considered as the *individuals* (ϕ_i) that are to be created,

$$\begin{aligned}\phi_i^1 &= (\beta_{1i} \quad \beta_{2i} \quad \beta_{3i} \quad \tau_i) \\ \phi_i^2 &= (\beta_{1i} \quad \beta_{2i} \quad \beta_{3i} \quad \beta_{4i} \quad \tau_{1i} \quad \tau_{2i})\end{aligned}\quad i = 1, \dots, N \quad (10)$$

There are basically two alternatives for the generation of the parameters that make up these individuals, ϕ_i^1 or ϕ_i^2 . The original GA approximation [Dawid (1999) or Arifovic and Gencay (2000) among others] is based on decomposing each number into a binary chain code, as *chromosomes*. A second alternative, Real-Coded GA, proposed by Davis (1989), is best suited for optimization problems of parameters with variables in continuous domains, and subsequently used by many authors [i.e.: Davis (1991); Wright (1991) or Eshelman and Shaffer (1993)]. In our case, we are going to use a version of the later in which each *chromosome* is identified by a random number generated through,

$$\beta_{ji} = \beta_j^* + \varepsilon_{ji} \quad i = 1, \dots, N \quad j = 1, \dots, 4 \quad (11)$$

$$\tau_{ji} = \tau_j^* + \varepsilon_{ji} \quad i = 1, \dots, N \quad j = 1, 2 \quad (12)$$

being β_j^* and τ_j^* the initial values around which the estimations are produced; and $\varepsilon_{ji} \sim N(0, \sigma_j)$. Herrera *et al.* (1998) show that this alternative has clear advantages in the case of numerical function optimization, since avoids coding and decoding processes needed in binary GA, increasing the computation speed; improves optimization efficiency in continuous domain problems without sacrificing precision as in alternate Gas and allows to exploit the smoothness of the optimization function.

We should stress that in this context the choice of initial values has no effect on the final estimation results, in contrast to Bolder and Strélski (1999) for traditional non-genetic algorithm based estimation methods. The objective in the context of genetic algorithms is to drastically reduce the computation time needed to reach the optimum solution.

¹⁰. In this case $N = 1200$.

To determine the possible values of β_j^* and τ_j^* we have implemented two complementary methodologies: the first uses initial values of the results of the estimation of the previous day; and the second is an approximation that takes into account the yield to maturity of assets with the shortest and longest term to maturity of all the assets with available prices for a particular trading day. The criteria for this second methodology are shown in table 1 (for the Nelson-Siegel model) and table 2 (for the Svensson). In practice, half of the individuals are created through each approximation, which allows us to use past estimations and current government bond market data simultaneously.¹¹

Table 1. Criteria used for establishing initial values of the Nelson and Siegel model (1987).

| Parameters | Initial value |
|------------|---|
| β_0 | Yield to maturity of the asset with least time until maturity. |
| β_1 | Difference between the yields to maturity of the assets with the least and most time until maturity. |
| β_2 | 0 (we assume there are no U or \cap shapes). |
| τ | Term to maturity of the asset with a closest yield to maturity to the halfway between β_0 and $\beta_0 + \beta_1$. |

Table 2. Criteria used for establishing initial values of the Svensson model (1994).

| Parameters | Initial value |
|------------|---|
| β_0 | Yield to maturity of the asset with least time until maturity. |
| β_1 | Difference between the yields to maturity of the assets with the least and most time until maturity. |
| β_2 | 0 (we assume there are no U or \cap shapes). |
| τ_1 | Term to maturity of the asset with a closest yield to maturity to the halfway between β_0 and $\beta_0 + \beta_1$. |
| β_3 | 0 (we assume there are no U or \cap shapes). |
| τ_2 | Equal to τ_1 |

Because of the specific characteristics of the models of the temporal structure of interest rates considered, the NSS functions, not every set of parameters generated is a valid solution, so with the N randomly generated individuals we proceed to test whether or not they are *viable*, i.e. if these parameters are coherent with an interest rate curve or not, eliminating

¹¹ Although similar survival capacity is reached if we only considered in each method, the speed of convergence to a final solution is improved with the use of a combination of initial values. Final results are a combination of individuals generated with both methodologies: around 2/3 of the parents comes from initial values fixed by estimation of previous days; and the rest of parents comes from initial values fixed with actual prices.

the genes that are not. With this step we considerably reduce the computation time and optimize the resources of later phases around viable solutions. The conditions to be met for an individual to be considered viable are,

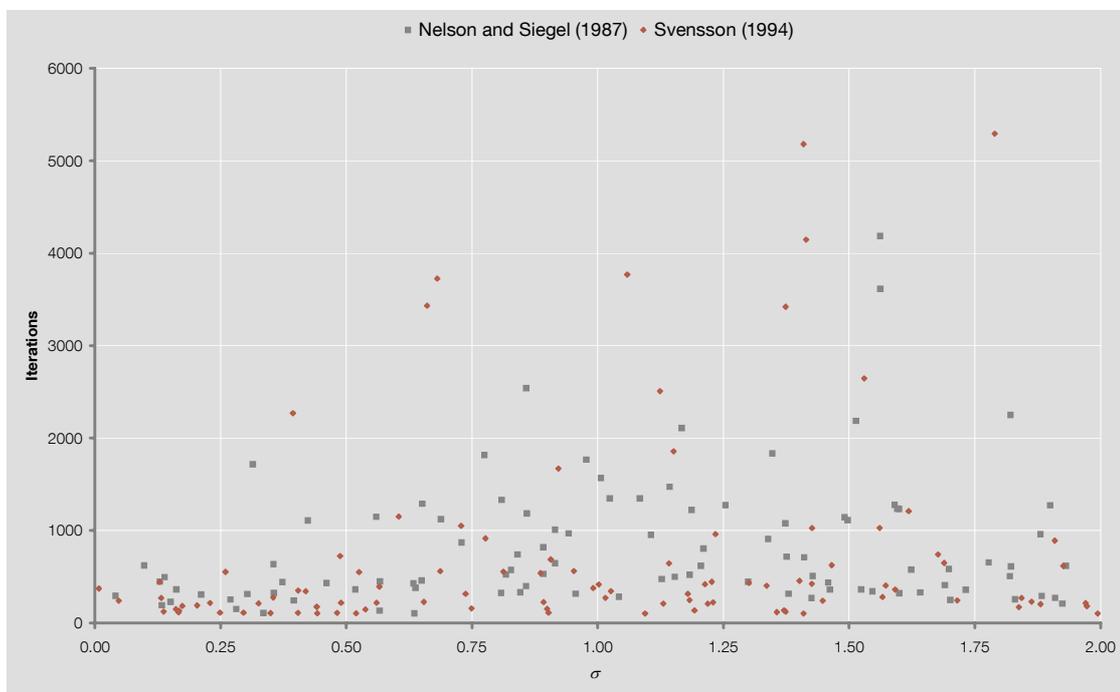
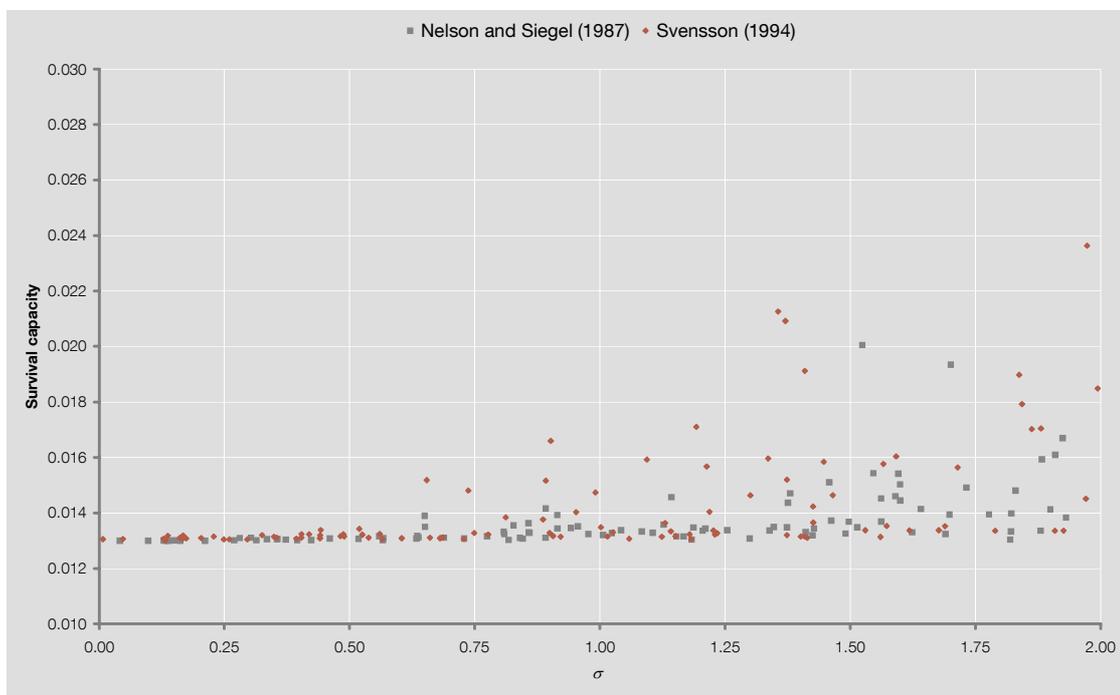
$$\begin{aligned} \beta_{1i} &> 0 \\ \beta_{1i} + \beta_{2i} &> 0 \\ \tau_{ji} &> 0 \end{aligned} \tag{13}$$

The variance of ε_{ji} ¹² allows for a wider variety of individuals in the first generation. But if the variance grows in excess, the values accepted by conditions stated in equation 13 is reduced, and the number of unviable individuals grows. If the final number of individuals in each generation is too low, then it is possible to end with a restricted generation instead of a wider one. The size of the variance has been selected¹³ from simulations presented in figure 4.

12. In this case, $\sigma_{\beta_0} = \sigma_{\beta_1} = \sigma\beta_0^*$; as they refer to interest rates; $\sigma_{\beta_2} = \sigma|\beta_2^*|$ and $\sigma_{\beta_3} = \sigma|\beta_3^*|$ as they refer to the parameters of intensity β_2 and β_3 when previous estimations are used or $\sigma_{\beta_2} = \sigma_{\beta_3} = \sigma|\beta_1^*|$ when β_2^* and β_3^* are equal to zero; finally, $\sigma_{\tau_j} = \sigma\tau_j$ as they refer to the parameters of speed of transition.

13. A final value of $\sigma = 0.5$ has been selected.

Figure 4. Simulations of the GA for different values of the standard deviation parameter (σ). Estimations of the term structure are made on January 9th 2004. Results are plotted against the SC and the number of iterations (generations) required to reach the minimum.



4.2 Selection

Once we have a large set of viable candidates, we can begin the selection process of these individuals. In this phase we choose the most appropriate genes for subsequent reproduction. In the context of the estimation of a model, the most appropriate is the parameter set that best fits the data, and would, therefore, be closer to the optimum.

To determine how appropriate an individual is we have to define a measure to quantify its *survival capacity* (SC). We use the goodness of fit of the curve to the data as an approximation of this survival capacity. In the term structure estimation context different measures of goodness of fit, generally based on the average squared error, have been proposed and used. The two most commonly used are based on the goodness of fit to either the asset prices or their yield to maturity. In the first case, the main drawback is that the same error in a bond price could represent very different fits in the term structure depending on the time to maturity of this bond. A small variation in price represents a very small change in interest rates if it belongs to a long-term bond and a more significant interest rate variation if it belongs to a short-term bond. This can be avoided by using the error in the bond yield to maturity instead of in bond prices, but it drastically slows down the algorithm so far as to make it prohibitive.

As a compromise between these two extreme alternative methods of quantifying the *survival capacity* (SC) we use the average squared error of the bond prices, which allows the algorithm to be reasonably fast and takes less computation time, but weighting every squared error by the inverse of the square root of its duration:

$$SC = \sum_{j=1}^k (P_j - \hat{P}(\phi_i))^2 \cdot \frac{1}{\sqrt{D_j}} \quad (14)$$

where k is the number of bonds used in the estimation of the curve on a particular day; D_i the Macaulay duration of these bonds; while $\hat{P}(\phi_i)$ is the bond prices computed through the term structure of interest rates determined by parametric set ϕ_i ,

$$\hat{P}(\phi_i) = \sum_{t=1}^n C \cdot e^{-s(t, \phi_i)t} + V \cdot e^{-s(m, \phi_i)m} \quad (15)$$

being C the coupon value, V is the nominal value of the asset and $s(t, \phi_i)$ is the spot interest rate at term t given a determined parametric set for individual i (ϕ_i).

The quantification of SC includes the weighting of prices in order to partially compensate for heterokedasticity. In fact, small changes in prices of short-term bonds imply great movements on interest rates, while in the long term we expect the opposite. So, by weighting for durations we give more relevance to the price errors of short-term issues, and it is usually applied to the Spanish term structure [Núñez (1996)].¹⁴ Nevertheless, along the sample we incorporate 6 references with terms of less than one year, so we have

¹⁴ An alternative procedure would imply defining the SC by the differences on yields instead of prices. Although this methodology avoids the problems of prices, it increases exponentially the computational time required to the estimation, and make it prohibitive for a genetic algorithm.

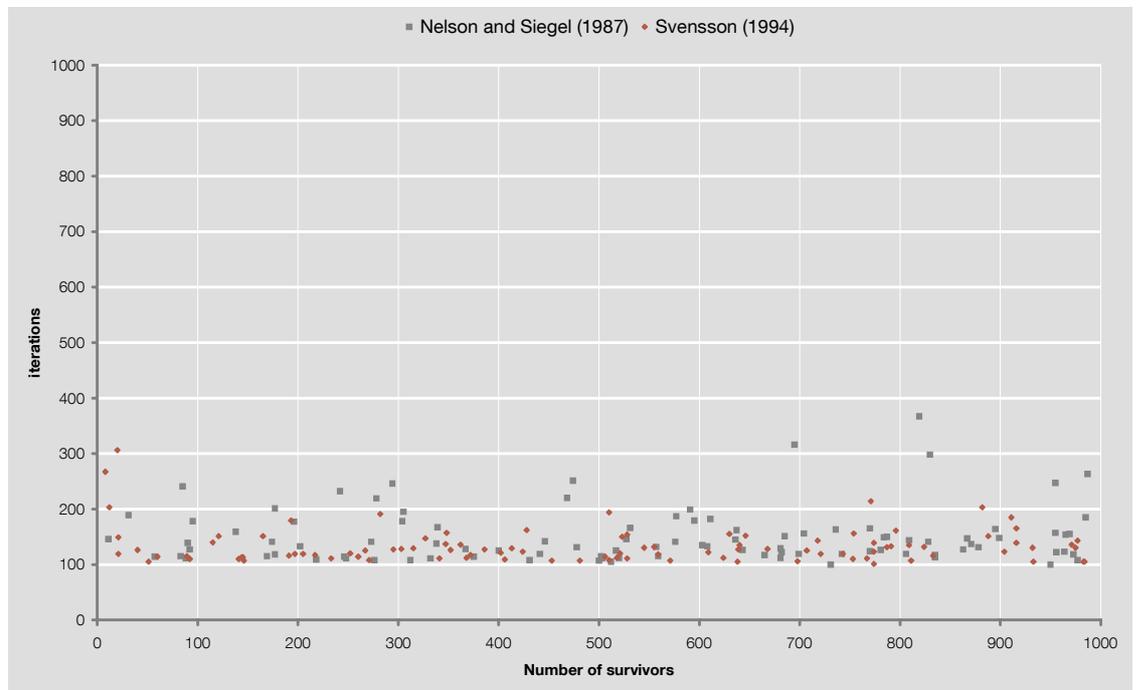
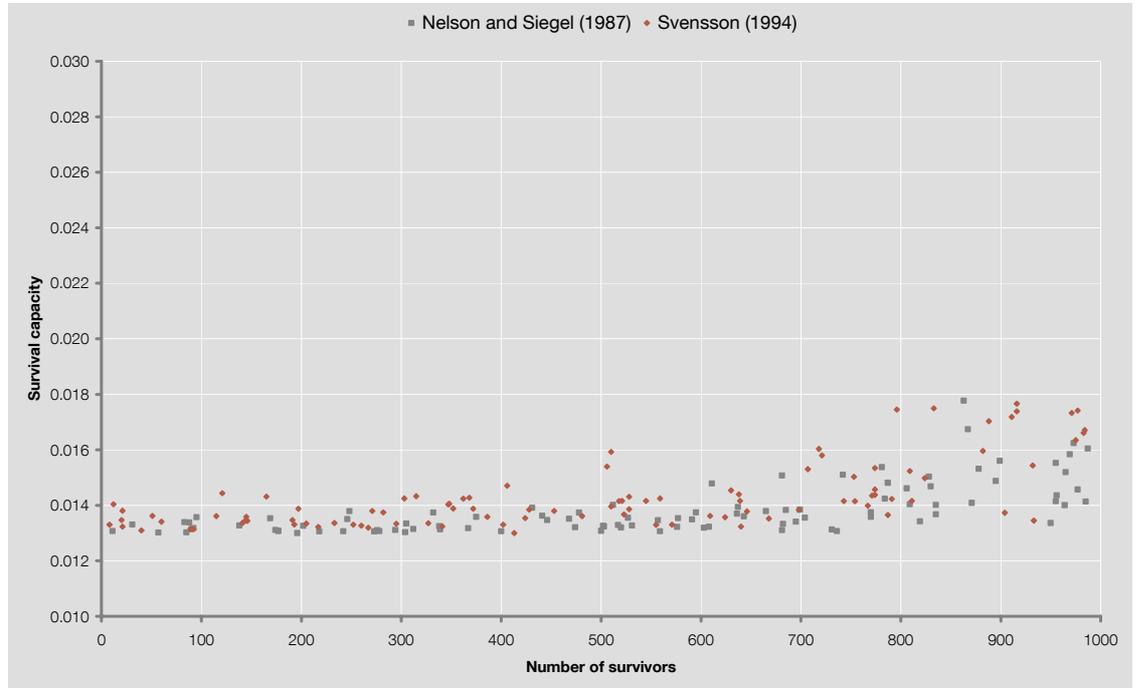
preferred the squared root rather than the level of durations in order to ensure that long term bonds played also a relevant role in the estimation process.¹⁵

This measure penalises the long-term bond prices in favour of the short-term bond prices in order to balance the goodness to fit along the term structure of interest rates. With this we overcome the drawback of using bond prices in the definition of the goodness of fit measure.

We consider that an individual has more survival capacity the lower the SC value. More concretely, in our case we consider that only 40% of the individuals will survive in each generation. This means that more than half of the individuals with the highest SC value (less goodness of fit) are eliminated in each iteration. If the number of survivors is too small, the process of convergence of the GA could be extremely slow, while on the contrary, if a sufficiently proportion of individuals are not removed the algorithm could leave us in a local minimum, since bad performance individual are not eliminated and less space is left for the new generations. Final value (40%) has been selected from initial estimations presented in figure 5.

¹⁵. In fact, short term issuances accounts for around 60% the weights, while the rest is evenly distributed between bonds with duration between 1-2 years, 2-5 years and more than 5 years.

Figure 5. Simulations of the GA for different values of the number of individuals that survive to each generation. Estimations of the term structure are made on January 9th 2004. Results are plotted against the SC and the number of iterations (generations) required to reach the minimum.



4.3 Cross-over and mutation

Once we identify the half of the *generation* that best approximates the curve, we have to try to improve the results. To this end we could use surviving individuals ϕ_i to obtain information on possible regions of the space in which we could find the parametric sets that fit best. This phase, in which we incorporate new candidates to be the optimum, is known as cross-over.

To incorporate the information provided by the previous phase, in which we calculated the SC of each individual, we complete the next generation creating *descendants* (ϕ_k) from two of the surviving individuals (ϕ_r and ϕ_s) of the previous generation. The descendant would therefore be a convex linear combination of the two progenitors,

$$\phi_k = \Psi \cdot \phi_r + (1 - \Psi) \cdot \phi_s \quad (16)$$

where Ψ is a column vector formed by uniform random variables in the interval [0,1] specific for each (r,s) pair. To select the progenitors of the new generation, we consider that the individuals with more survival capacity will be those with the most probability of reproducing. Therefore, r and s , are selected thus,

$$r, s = N \cdot \xi \quad \xi \sim \mathbf{B}(1, \alpha) \quad (17)$$

being N the size of each generation and ξ a random variable with a Beta distribution with parameters 1 and α . The larger this last parameter, the greater the probability of lower values, so α can be interpreted as an indicator of the *attractiveness* conceded to those genetically better individuals. If α is too low, then no predilection is made for the best fitted individuals and the GA fail to reach an acceptable minimum. On the contrary, if α is excessively high, then not enough diversity will remain on each generation, and the convergence process will be slowed down (see figure 6). A compromise between these considerations is made, and the attractiveness parameter is settled to be $\alpha = 6$.

In the creation process of new individuals, this procedure allows the algorithm to account for the goodness of fit attained by the individuals of the previous generation, with a bias in favour of parameter values that have attained better results in approximating the shape of the curve. This bias has to be equilibrated, as it is not good for the convergence to be too quick, which would once again trap the algorithm in a local minimum.

After the cross-overs, we have to consider the possibility of *mutations*, which allow us to ensure that the function is not stuck in a local minimum. To do this, every parameter of each individual can suffer a mutation with a given probability (π). When this happens, a variable $\varepsilon_{ji} \sim \mathbf{N}(0, \sigma_i)$ is added to the mutated parameter. These mutations are independent on each parameter, so in a given individual you could have zero, one, two... parameters mutated. Lower values of π reduce the speed of convergence of the model, since the optimization is mainly based on crossover slowing down the process, while if a high π is settled, mutation will be the dominant driver of the algorithm and there will be no sure convergence to an optimum (see figure 7). A compromise is reached for $\pi = 0.35$.

Figure 6. Simulations of the GA for different values of the attractiveness parameter (α). Estimations of the term structure are made on January 9th 2004. Results are plotted against the SC and the number of iterations (generations) required to reach the minimum.

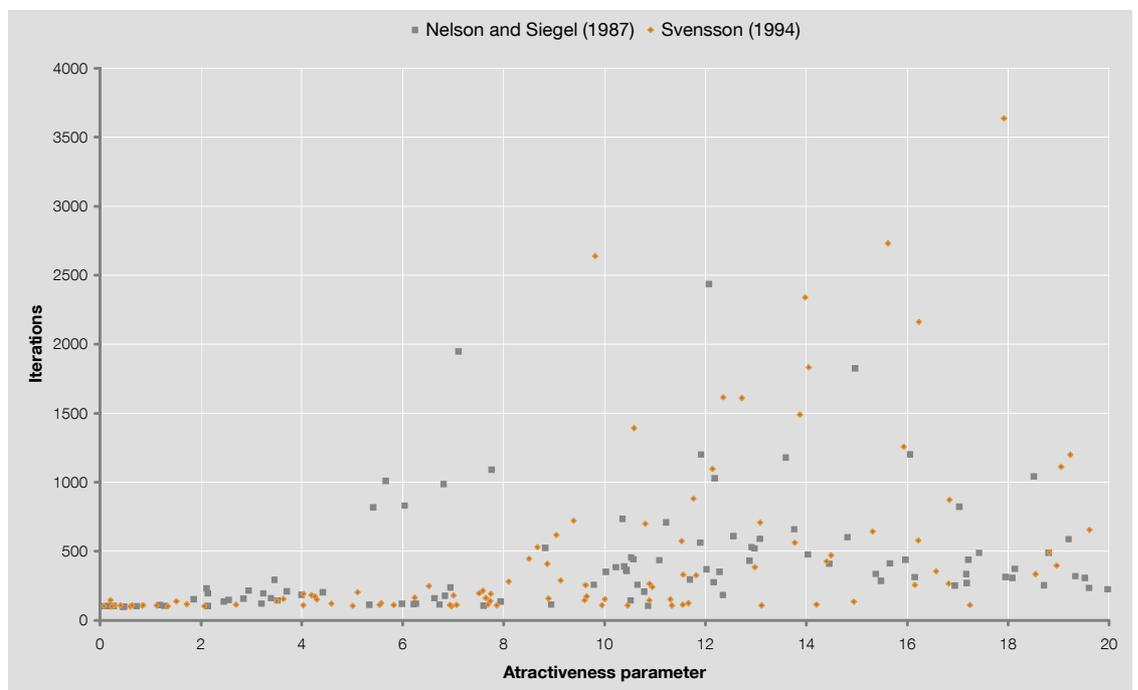
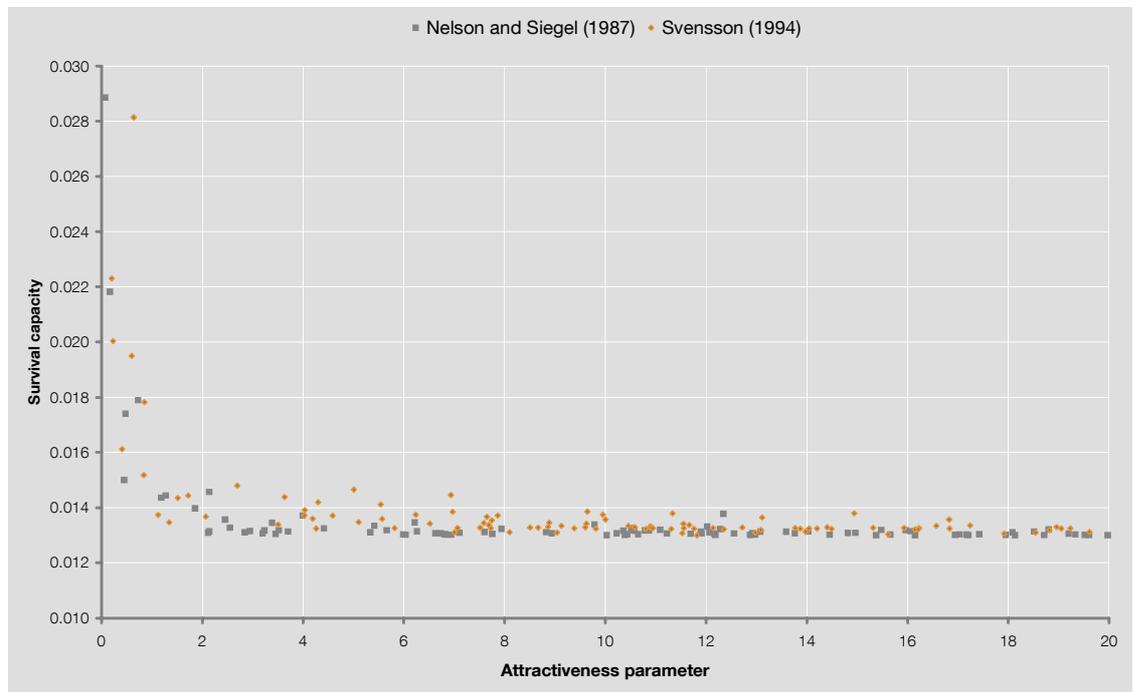
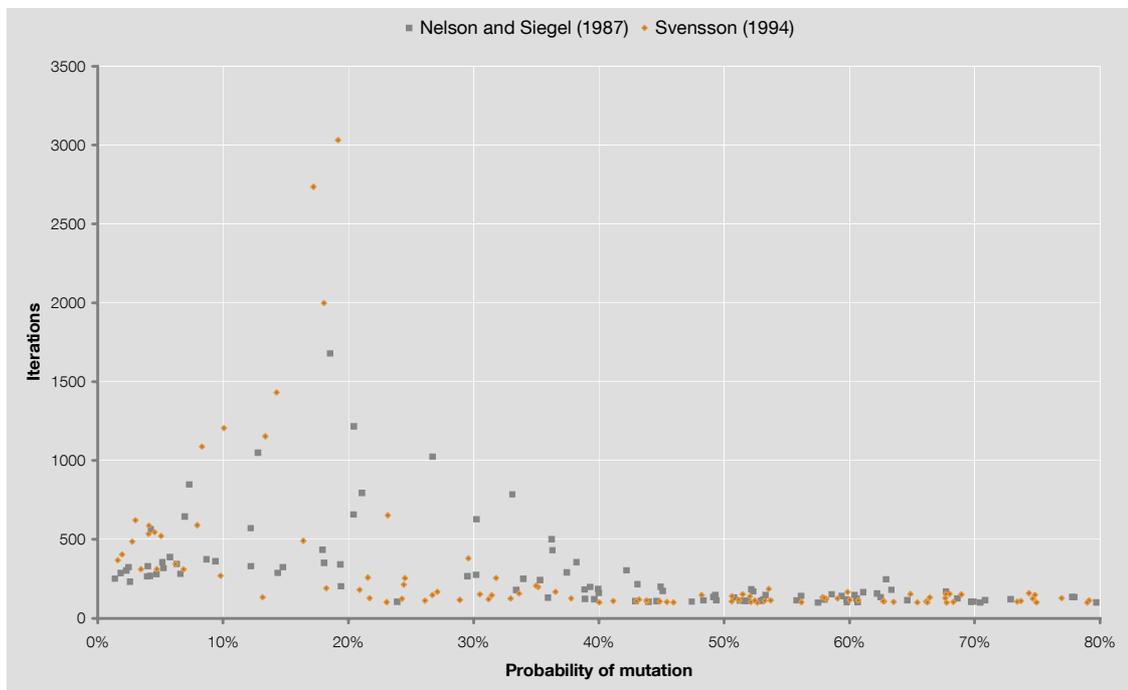
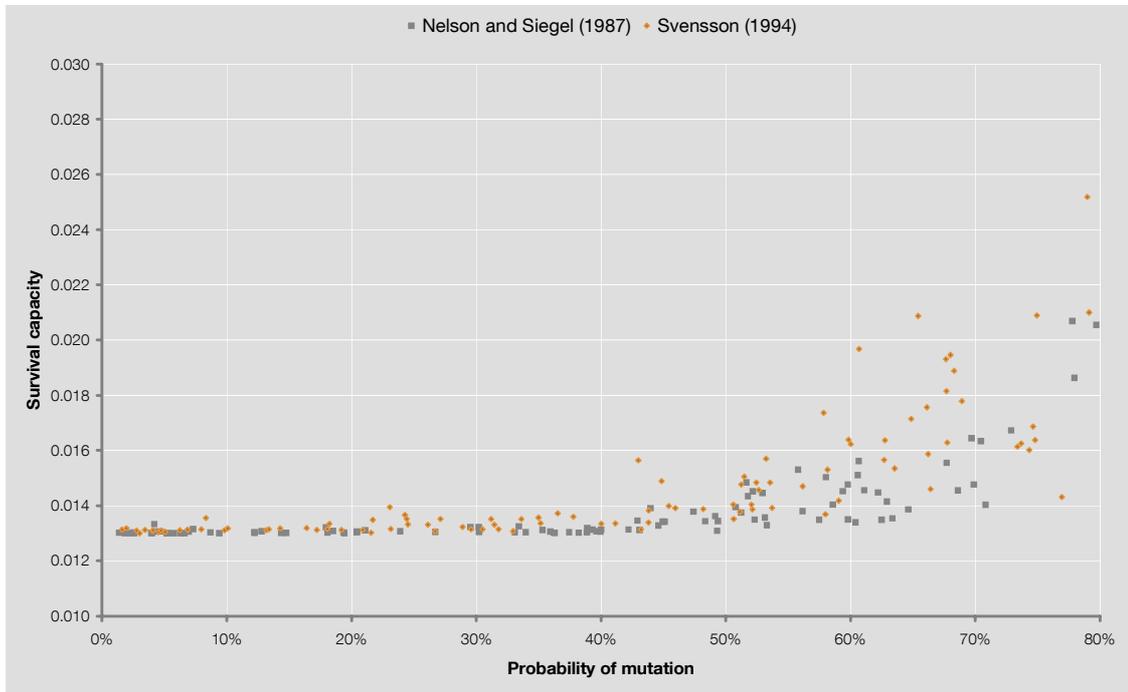


Figure 7. Simulations of the GA for different values of the probability of mutation (π). Estimations of the term structure are made on January 9th 2004. Results are plotted against the SC and the number of iterations (generations) required to reach the minimum.



The magnitude of each mutation is given by σ , which we make increase with each generation.¹⁶ We have decided that the standard deviation will not be constant because although there are quick improvements in the optimum with a constant standard deviation, the form of the function makes it extremely easy for the algorithm to stop in a local minimum, so that by increasing the variability of the mutations realized we make the algorithm easily jump towards depressions with lower local minimums.

Once we have completed a generational leap, we return again to testing the viability of the new generation and its survival capacity. This process is repeated iteratively until we obtain a series of 100 generations without changes in the individual with greater probability of survival. This means that the number of generations (iterations) needed to estimate the parameters of the curve is not a fixed number, making it difficult to give estimations of the computation time required for the algorithm, because it would vary a lot from day to day, or even from one implementation of the algorithm to another. The main advantage is that the final result of the estimation is much better, and much more stable from one day to the next.

Convergence with the GA is quite fast, and requires a sort number of generations (iterations) to reach acceptable results (around 50 iterations). Our non-fix number of generation procedure just ensures that a better result not has been overlooked, extending to between 500 to 2000 iterations, and no more than five minutes of matlab processing in a standard Pentium4-PC. Nelson and Siegel (1987) function is less time consuming with a faster convergence and a lesser number of generations are required than Svensson (1994) function, when 2 more parameters are needed to be estimated.

4.4 Results

In figure 8 we compare the goodness of fit (SC) achieved in the period from January 2004 to February 2005 with the traditional optimization method and with genetic algorithms for the Nelson and Siegel (1987) and the Svensson (1994) functions. We find that the results obtained with genetic algorithms are notably superior in fit capacity and stability. It should also be noted that the chosen sub-period corresponds with a time in which this measure was not especially high for the traditional estimation of the curve.

An additional advantage of the use of genetic algorithms (GA) revolves around the stability and trustworthiness of the parameters obtained, as can be seen in figure 9. In this figure we see how the GA estimations remove the violent swings and anomalous values which characterise temporal series of interest rates.

Moreover, as can be seen in figure 10, that represents the evolution of β_2 and β_3 , the differences in the behaviour of this parameters in GA and traditional estimations are easy to see. While traditional estimation gives opposite values for both parameters, implying that they play a minor role in the behaviour of the whole term structure, GA estimation clearly shows that both parameters have independent values effectively taken into account distortions in the evolution of the curve from the very short-term to the very long-term interest rate. This allows us to make use of the capabilities of the Svensson equation (1994) to adapt to more elaborate curve shapes.

¹⁶. Parameter σ_t is settled for the first generation to be equal to the standard deviation used in equations 11 and 12. For the following generations the value is increased by a 2%.

Figure 8. Comparison of the average squared error committed with the nonlinear Svensson estimation obtained with the traditional optimization method and the genetic algorithms estimations made on the Nelson and Siegel and Svensson functions.

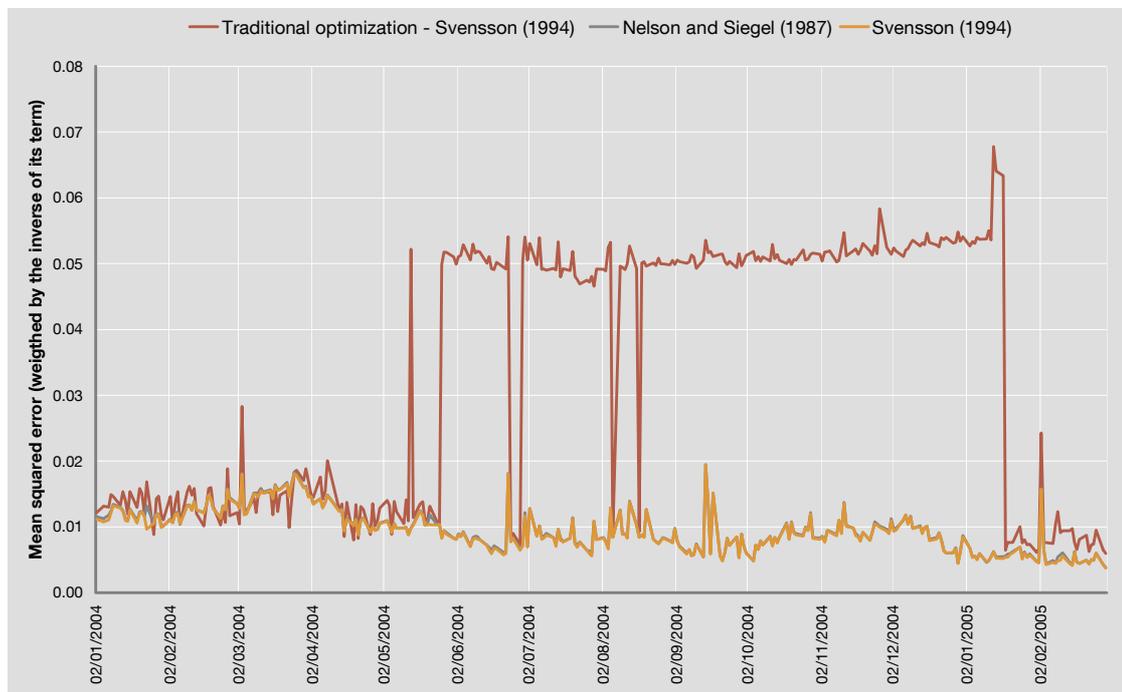


Figure 9. Temporal evolution of the long-term interest rate (top) and the short-term (bottom) from 2/01/2004 to 1/03/2005 measured through the estimation of β_0 and $\beta_0 + \beta_1$ with genetic algorithms [using both the Nelson and Siegel (1987) function and the Svensson (1994) function] and with a traditional nonlinear algorithm [Svensson (1994)].

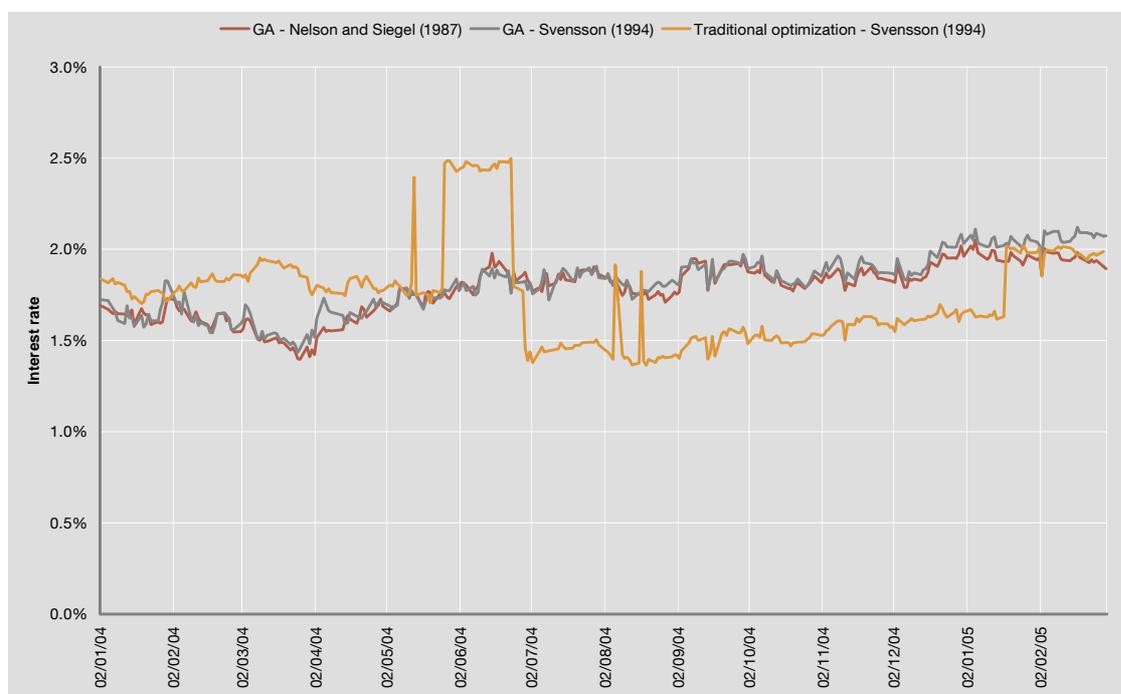
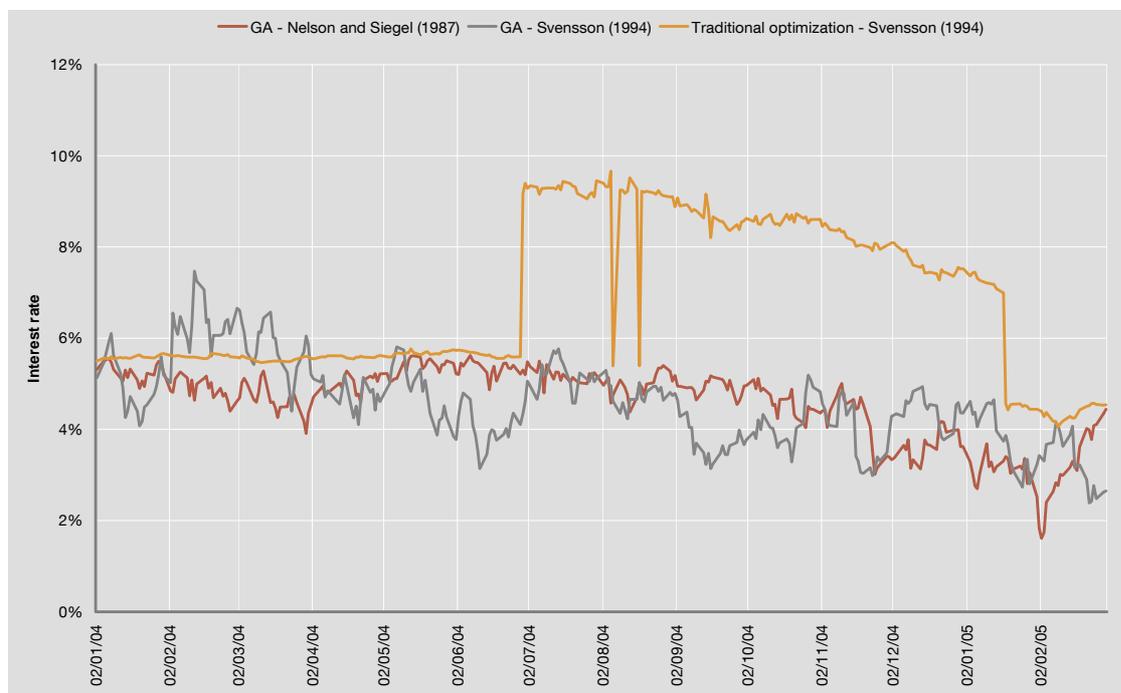
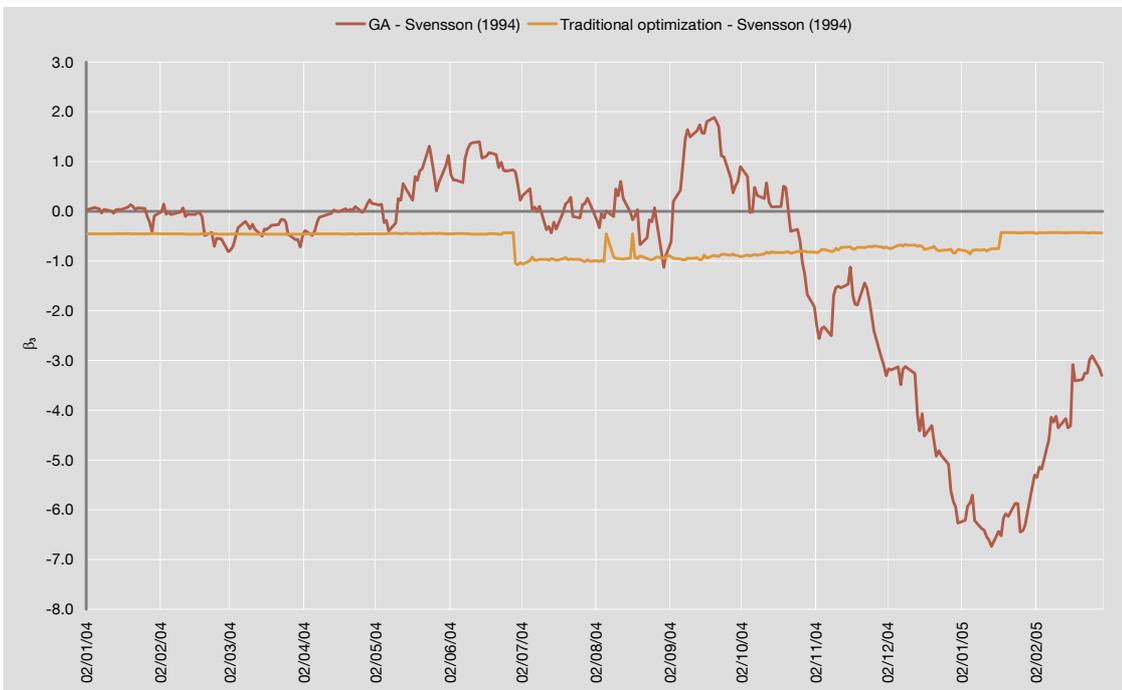
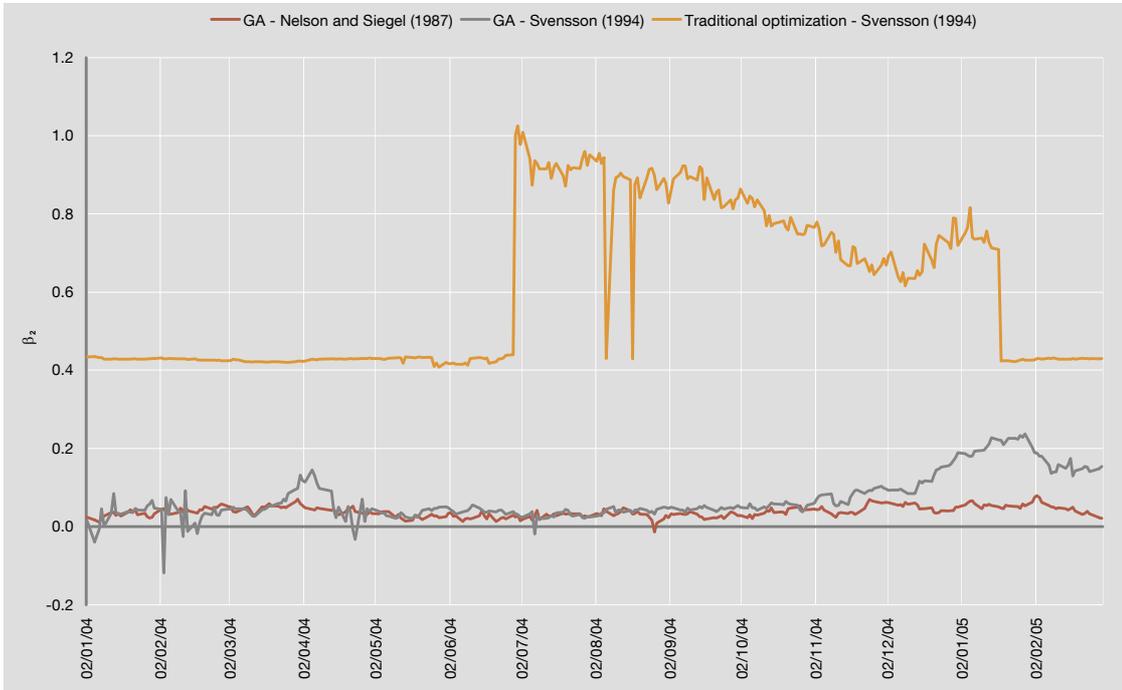
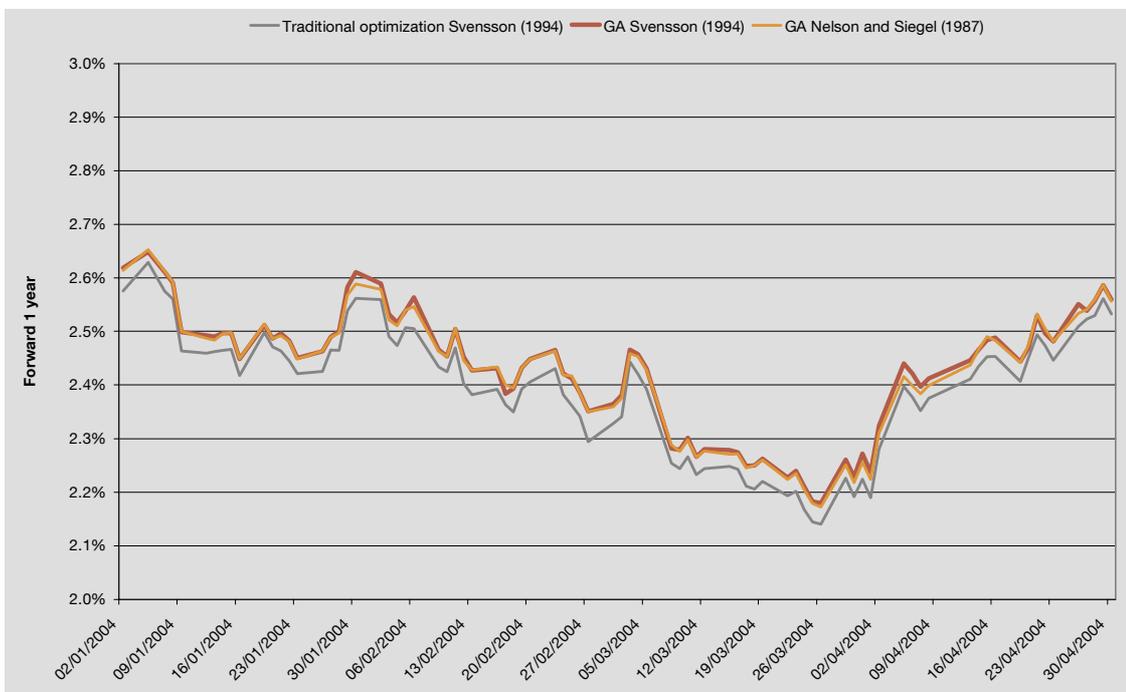
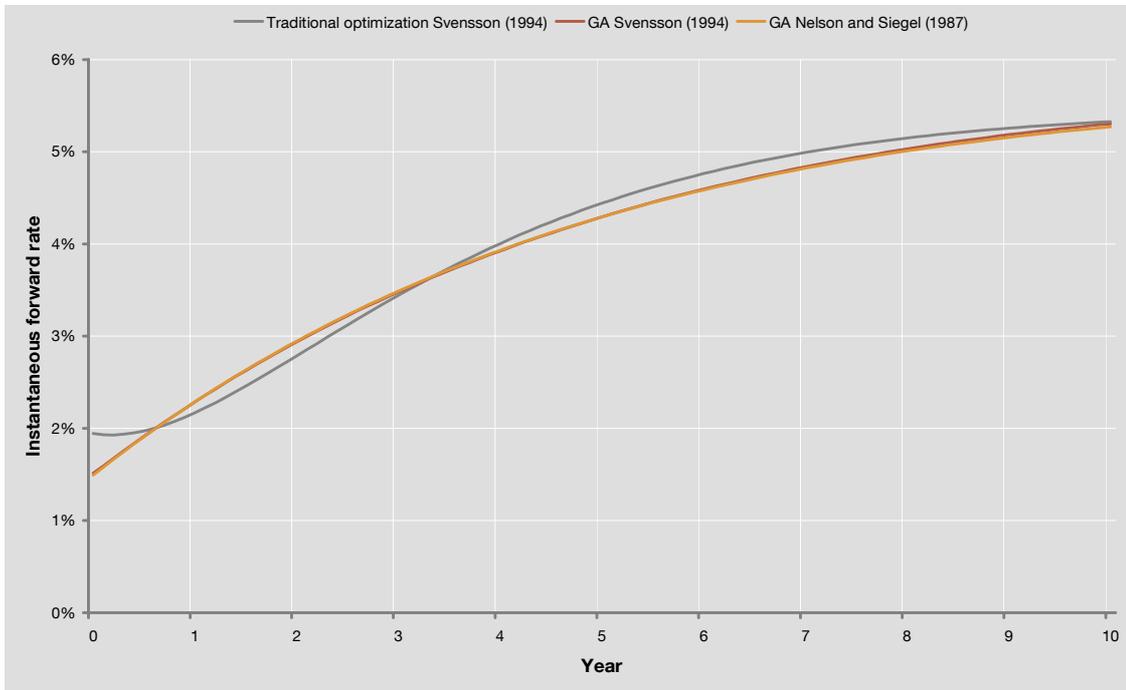


Figure 10. Temporal evolution of the parameters of intensity β_2 (top) and β_3 (bottom) from 2/01/2004 to 1/03/2005 measured through estimation with genetic algorithms [using both the Nelson and Siegel (1987) function and the Svensson (1994) function] and with a traditional nonlinear algorithm [Svensson (1994)].



Even when estimations obtained from traditional optimization methods get similar fitting results than a GA estimation, results are quite different. The difficulties in the determination of the parameters of traditional methodologies imply that spot, and specially forward term structure are quite different. In the temporal sample considered, the period of January-April 2004 gives similar fitting results, but instantaneous forward rate is completely different to GA estimations (see figure 11). In fact, forward one year interest rate is systematically underestimated along the period, and also more unstable.

Figure 11. Instantaneous forward rate term structure for March 13th, 2004 (top) and temporal evolution of the forward 1 year interest rate from 2/01/2004 to 30/04/2006 (bottom), both estimated with genetic algorithms [using both the Nelson and Siegel (1987) function and the Svensson (1994) function] and with a traditional nonlinear algorithm [Svensson (1994)].



5 Conclusions

The relevance of the term structure of interest rates in finance but also in macroeconomics, justifies its estimation by the central banks of the major economies. To do this, these institutions implement methodologies appropriate to the required use of the term structure estimated. In this context, fitting through the Nelson-Siegel-Svensson functional forms is the most widely used methodology and, therefore, merits special attention in order to solve the problems deriving from its implementation.

One of these problems is the instability of the parameters estimated. This instability is especially caused by the need to arbitrarily fix the initial values in the fitting process of the curve with traditional optimization methods. This problem, which has been fully documented in this article, becomes especially important when we want to economically interpret the estimated values of the parameters of the fitted functions, and even more so when the dynamic behaviour of these parameters is used, as found in the literature, as risk factors in bond risk-return models.

In this paper we have proposed the use of genetic algorithms as an alternative optimization methodology to the traditional methods. This methodology has the advantage of not having results that depend on the initial values used and from this we expect its implementation to minimize the risk of non-convergence and consequently obtain better fitted estimations as well as greater stability in the parameters that determine the fit. In this way, the results obtained in this paper can not be any more promising as they confirm these expectations and, furthermore, show how the implementation of the proposed methodology avoids compensation among the estimated values of different parameters of the NSS functions, giving them back their original economic interpretation.

Although genetic algorithms are more computationally intensive than traditional parametric estimation, this is not a limitation nowadays. In fact, a reasonable optimum is reached in between 500 to 2000 iterations that requires less than five minutes of a standard PC.

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