A determination of $\alpha_s$ from scaling violations with truncated moments
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We describe a determination of the strong coupling $\alpha_s(M_Z)$ from scaling violations of the nonsinglet DIS structure function, which is based on two novel techniques aimed at controlling and minimizing the theoretical error: a neural network parametrization of BCDMS and NMC data, and QCD evolution by means of truncated Mellin moments.

1. Introduction

Scaling violations of DIS structure functions play a key role in our understanding of perturbative QCD, and their measurement is one of the most natural and potentially cleanest methods available for the determination of the strong coupling $\alpha_s$. There are, however, practical and conceptual difficulties that must be overcome to achieve with this method a precise determination of $\alpha_s$ and its associated statistical and theoretical errors.

The theoretical prediction for scaling violations is given by Altarelli–Parisi evolution equations. A clean, analytic solution at NLO in the coupling is available in terms of Mellin moments of structure functions, which diagonalize the evolution operator. The difficulty in the implementation of this solution is the fact that moments are not directly measurable, since they are weighted integrals of the structure function over the interval $0 < x < 1$, and $x \to 0$ implies $\sqrt{s} \to \infty$. The uncertainty on the value of any given moment is thus unknown, and in principle infinite: it is necessary to rely upon extrapolations. An alternative, practical, if less elegant method of solution is to work numerically, directly with the $x$–space integro–differential equation. This involves, in principle, no extrapolation, since AP evolution is directional in $x$ space, however it can be numerically challenging. Furthermore, in practice, this method usually requires the introduction of a parton parametrization, and this raises new issues: in fact, the choice of a parametrization is a source of theoretical bias, very difficult to assess, and errors on physical observables associated with the parametrization are notoriously difficult to evaluate.

Our goal here is to present a data–driven determination of $\alpha_s$, which tackles the problems outlined above. We use BCDMS and NMC data for the nonsinglet DIS structure function $F_2$, and we strive to minimize all sources of theoretical bias and uncertainty, while accurately assessing the statistical effects of experimental errors and correlations.

To this end, we employ two theoretical tools which have recently been developed. First, we solve AP equations by means of truncated Mellin moments; next, we make use of a bias–free parametrization of $F_2$, constructed by means of neural networks.
Mellin moments over a truncated interval \((x_0 < x < 1)\) are observable quantities; as shown in Ref. \[8\], they obey a simple evolution equation, which can be approximated with arbitrary precision by a matrix equation admitting a simple analytic solution. In principle, since one is manipulating observable quantities, a parametrization of the structure function is not needed. In practice, however, data coverage and precision are not sufficient, and to extract from the data the maximum amount of information (for example, in order to combine errors on neighboring data points in the best way) it is necessary to impose the constraint of continuity on the structure function, i.e. to introduce a parametrization. To do so without introducing a theoretical bias, and keeping full control on the propagation of experimental errors and correlations, we make use of the results of Ref. \[8\], where neural networks were employed in conjunction with Monte-Carlo techniques to construct a faithful representation of the probability distribution in the space of structure functions.

2. Evolution with truncated moments

Truncated Mellin moments of a parton distribution \(q(x, t)\), with \(t = \log \mu^2\), are defined by

\[
q_n(x_0, t) = \int_{x_0}^1 dx\ x^{n-1} q(x, t).
\]

They satisfy the evolution equation

\[
\frac{dq_n}{dt} = \frac{\alpha_s}{2\pi} \int_{x_0}^1 dy\ y^{n-1} q(y, t) G_n \left( \frac{x_0}{y}, \alpha_s \right),
\]

where

\[
G_n(x, \alpha_s) = \int_z^1 dz\ z^{n-1} \mathcal{P}(z, \alpha_s)
\]

is the truncated moment of the appropriate AP kernel \(\mathcal{P}(z, \alpha_s)\).

As \(x_0 \to 0\), \(G_n\) becomes the anomalous dimension \(\gamma_n\), and different moments evolve independently; for \(x_0 \neq 0\), evolution couples the \(n\)-th truncated moment \(q_n\) with all other \(q_k\), with \(k > n\), as easily seen by Taylor expanding \(G_n(x_0/y)\) around \(y = 1\). This Taylor expansion converges in the interval \(x_0 < y \leq 1\), since \(G_n\) only has integrable singularities due to + distributions at \(y = x_0\). Truncating the expansion at the \(M\)-th term yields the linear system

\[
\frac{dq_n}{dt} = \frac{\alpha_s}{2\pi} \sum_{p=0}^M c^{(M)}_{p,n}(x_0, \alpha_s) q_{n+p}(x_0, t),
\]

with coefficients that can be computed analytically to the order to which the splitting functions are known.

Methods for the solution of Eq. (2.4) and their accuracy have been studied in Refs. \[7,9,10\]. One may first of all observe that the matrix of anomalous dimensions governing the evolution of truncated moments is upper triangular. As a consequence, it can be diagonalized analytically by means of a simple recursion relation. A second observation is that moments with significantly different indices are weakly coupled for small \(x_0\). This is what justifies the truncation of the expansion of the r.h.s. of Eq. (2.4) at finite \(M\).

The convergence of the series of approximations for increasing \(M\) has been studied systematically. The convergence of the approximation as a function of \(M\) is good (leading to a few percent error for \(M \lesssim 20\)), except for lowest nonsingular moments (sensitive to singularities at \(y = x_0\)). An improved version of the method \[10\] deals with this problem, so that in fact for all finite moments \(M \lesssim 12\) is sufficient to achieve an accuracy on evolution at the percent level.

The method has also been extended to singlet and gluon distributions \[9\], with minor technical complications; a NLO analytic solution is available in all cases and can be efficiently implemented numerically (for details, see \[11\]). It is worth emphasizing that, being based on Mellin moments, the method is also well suited to include the effects of threshold logarithms, which may in fact play a non-negligible role in the determination of \(\alpha_s\).

3. Neural network parametrization of \(F_2\)

The standard procedure for fitting structure functions, as well as parton distributions, is to choose a simple functional form with enough free parameters, and then fix the value of the parameters by minimizing a suitable \(\chi^2\). This proce-
To solve these problems, what is needed is a reliable representation of the probability measure \( \mathcal{P}(F_2) \) in the space of structure functions \( F_2(x, Q^2) \). Then, for any observable functional \( \mathcal{G}(F_2) \), one could compute

\[
\left\langle \mathcal{G}[F_2] \right\rangle = \int \mathcal{D}F_2 \, \mathcal{G}[F_2(x, Q^2)] \, \mathcal{P}(F_2),
\]

and similarly for higher moments. Just such a representation was constructed, using a combination of Monte–Carlo techniques and neural networks, in Ref. [8].

Neural networks are a class of algorithms providing robust, universal and unbiased approximants to incomplete or noisy data. As such, they are ideally suited to handle problems like the ones discussed above, which center on the need to reconstruct a continuous function from a discrete set of data with errors.

Space prevents us from discussing here in any detail the technology of neural networks, their properties and applications (for an introduction, see for example Ref. [14]). For the record, the neural architecture implemented in Ref. [8] is that of a multilayer feed–forward network or “perceptron”. This means that network nodes (neurons) are arranged in an ordered sequence of layers, and each neuron receives input from the neurons in the preceding layer, while feeding output to those in the successive layer. The network learns to interpolate the chosen set of data by the method of supervised training by back–propagation. In practice, the network attempts matching data to output, then proceeds to vary the parameters characterizing neuron activation (weights and thresholds), along the steepest descent contour, searching for the minimum of the chosen error function.

The only assumption made by the network algorithm is that the data can be interpolated by a smooth function. All the parameters characterizing the network, such as size (number of neurons), architecture (structure of layers), length of the learning cycle, can be decided based on purely statistical criteria. Specifically, no assumption is made on the functional form of the interpolating function.

The parametrization of the nonsinglet structure function \( F_2^{(NS)}(x, Q^2) \) constructed in Ref. [8] is based on a total of 552 data points collected by the NMC and BCDMS collaboration. The method used is a combination of Monte–Carlo techniques with neural network technology, and consists of two steps. The first step is the Monte–Carlo generation of an ensemble of \( N_{\text{rep}} \) pseudo–data sets, mimicking the real data, with the correct multivariate distribution given by experimental errors, fully correlated. Let \( i \equiv \{x, Q^2\} \) be a point where \( F_2^{(NS)}(x, Q^2) \) has been measured, obtaining the result \( \mathcal{F}_i^{(exp)} \), with statistical error \( \sigma_i \), normalization error \( \sigma_N \) and percentage systematic errors \( f_{i,a} \). Then one generates the \( N_{\text{rep}} \) pseudo–data at point \( i \) according to

\[
\mathcal{F}_i^{(art)}(k) = \left( 1 + r_{i,N}^{(k)} \right) \mathcal{F}_i^{(exp)} + \sum_a r_{i,a}^{(k)} f_{i,a} \frac{\sigma_i \sigma_N}{100},
\]

where \( k = 1, \ldots, N_{\text{rep}} \), and \( r_{i,a}^{(k)} \) are univariate gaussian random numbers, which for systematic errors are grouped in classes according to experimental correlations.

The second step is the training of \( N_{\text{rep}} \) neural networks, each one using one pseudo–data set. At the end of training, the parameters of each network are optimized for the interpolation of the
corresponding data set; the output of the process is a set of \( N_{\text{rep}} \) continuous functions \( F^{(k)}(x, Q^2) \) representing a faithful sample of the probability distribution \( P(F_2) \).

Finally, one may evaluate averages, errors and correlations of observables using the \( N_{\text{rep}} \) networks as a Monte–Carlo representation of \( P(F_2) \). In this context, \( \alpha_s \) can be treated like any functional of the structure function.

4. Fit architecture and parameters

Having at our disposal the ensemble of structure functions needed for the analysis, there are still a number of parameters that may be chosen in the fitting procedure to determine \( \alpha_s \), to maximize the accuracy of the results. First of all, we must choose the truncation point \( x_0 \) entering the definition of truncated moments, Eq. (2.1), as well as the fitting range in \( Q^2 \). The criteria for these choices are simple: we must take maximal advantage of data coverage, in order to minimize statistical errors on individual moments; we must impose a lower cut on \( Q^2 \) to keep power correction under control; we must keep \( x_0 \) as small as possible, compatibly with data coverage, to ensure a fast convergence of our approximate evolution equation. We also have a choice regarding the number of intermediate scales to be used as evolution targets: in principle we could apply the evolution equation between any two scales in the fitting range, however introducing too many intermediate scales would clearly not add new information, and it would lead to large correlations between neighboring moments. Based on these criteria and extensive testing, we choose \( x_0 = 0.03 \) for the truncation point, \( 20 \ \text{GeV}^2 < Q^2 < 70 \ \text{GeV}^2 \) for the fitting range, and \( n_{\text{net}} = 3 \) for the number of scales, which are taken to be equally spaced on a logarithmic scale.

A second set of choices to be made concerns our approximate evolution equation. We work with a NLO evolution equation with matching at heavy quark thresholds according to the Marciano prescription [15]; we must then decide how many truncated moments should be included in the evolution to achieve a satisfactory accuracy while preserving numerical stability. An optimal choice is to include truncated moments with \( 1 \leq n \leq 11 \), i.e., to set \( M = 11 \) in Eq. (2.2). Since we are including the lowest nonsingular moment, we must use the improved method of solution described in Ref. [15]; the auxiliary parameter introduced there is set to \( N = 6 \). We performed several tests on our approximate solution with these parameters, and found that the accuracy achieved on evolution in the relevant range is at the level of 0.1%.

A final important issue is the number of moments that should be treated as fit parameters together with the strong coupling. In fact, the values of truncated moments at the target scales of perturbative evolution depend both on the coupling and on the values of the same moments at the initial scale. These initial values can be either fixed at the central experimental value, or fitted. It turns out that to achieve a satisfactory precision, given the statistical errors on truncated moments, the number of fitted moments must be \( n_{\text{fit}} > 3 \). On the other hand, fitting a large number of moments, especially successive ones, endangers the numerical stability of the fit due to the very large correlations between neighboring moments. This forces \( n_{\text{fit}} < 6 \). After testing the possible combinations, we find that the choice that minimizes errors while maintaining numerical stability is to fit moments \( n = 2, 4, 5, 6, 8 \).

We emphasize that all fit parameters have been varied within their respective windows of stability with negligible effects on the results.

5. Result and errors

As shown in Ref. [8], an ensemble of \( N_{\text{rep}} = 1000 \) networks is sufficient to reproduce correctly all experimental errors and correlations, without introducing any bias. With such an ensemble, and the fit architecture outlined above, our result with statistical errors is

\[
\alpha_s(M_Z) = 0.124 \pm 0.004 \text{ (stat.)}.
\]  

(5.7)

Theoretical uncertainties remain to be estimated. A first source is the presence of power correction, which are not accounted for by a perturbative treatment. They can be of a kinematical nature (target mass corrections), or dynamical (higher
twist corrections), or due to elastic contributions at \( z = 1 \). As discussed in Ref. [3], all are found to be negligible (<1%) thanks to our choice of \( Q^2 \) range. A second source of theoretical error is given by the uncalculated NNLO and higher perturbative contributions to the evolution equation. These can be estimated by varying the renormalization scale according to \( \mu^2_{\text{ren}} = k_{\text{ren}}Q^2 \) (note that there is no factorization scale dependence in DIS scheme). We have tested the range \( 0.3 < k_{\text{ren}} < 4 \), and found that the ensuing uncertainty is not negligible, indicating sizeable NNLO corrections: \( \sigma_{\text{ren}} = 0.003 \). It is conceivable, and it can be tested, that our method might be affected by an enhancement of threshold logarithm effects, since the fitting procedure involves relatively high Mellin moments. The inclusion of such logarithms in a resummed fit should be natural with our formalism, since resummation is performed in Mellin space, where our evolution takes place. A final possible source of theoretical error is the location of heavy quark thresholds. This is estimated by varying the threshold position as \( Q^2_{\text{th}} = k_{\text{th}}M^2_\tau \), with \( 0.3 < k_{\text{th}} < 4 \). The effect is expected to be nearly negligible, since only the \( b \) threshold is included in our \( Q^2 \) range, and only for some \( k_{\text{th}} \). We find in fact that \( \sigma_{\text{th}} = 0.003 \). Summarizing, our final result for the strong coupling reads

\[
\alpha_s(M_Z) = 0.124 \pm 0.003 \text{ (exp.)} - 0.004 \text{ (th.).} \tag{5.8}
\]

We observe that the error is dominated by statistical uncertainties, consistently with our expectations. The central value turns out to be somewhat on the high side of the current world average, though well within errors. We note that this is consistent with the possibility that threshold logarithms might affect our determination more than others, since it is known that their leading effect is to replace the argument of the coupling, changing \( Q^2 \) to \( Q^2/n \) for the \( n \)-th moment, thus leading to a larger value for the effective coupling.

Resummation of soft gluon effects will probably lead to a further reduction of the theoretical error, which is dominated by unknown higher order corrections. On the experimental side, the result could be significantly improved either with better statistical accuracy (particularly of deuteron data), or by extending the range in \( Q^2 \), which might be achieved by the planned EIC facility [18].

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**REFERENCES**

[1] S. Bethke, hep-ex/0004021, J. Phys. G26 (2000) R27.
[2] G. Altarelli and G. Parisi, Nucl. Phys. B 126 (1977) 298.
[3] See e.g. S. Alekhin et al., hep-ph/0204316, in Les Houches 2001, Proceedings.
[4] S. Forte, J.I. Latorre, L. Magnea and A. Piccione, Nucl. Phys. B 643 (2002) 477, hep-ph/0205286.
[5] A.C. Benvenuti et al., Phys. Lett. B223 (1989) 485; Phys. Lett. B237 (1990) 592.
[6] M. Arnesano et al., Nucl. Phys. B483 (1997) 3, hep-ph/9610231.
[7] S. Forte and L. Magnea, Phys. Lett. B 448 (1999) 295, hep-ph/9812473.
[8] S. Forte, L. Garrido, J.I. Latorre and A. Piccione, hep-ph/0204232, JHEP 0205 (2002) 062.
[9] S. Forte, L. Magnea, A. Piccione and G. Ridel, hep-ph/0006273, Nucl. Phys. B 594 (2001) 46.
[10] A. Piccione, Phys. Lett. B518 (2001) 207, hep-ph/0107108.
[11] A. Piccione, hep-ph/0207204.
[12] S. Forte, Nucl. Phys. A666 (2000) 113.
[13] W.T. Giele, S.A. Keller and D.A. Kosower, hep-ph/0104053.
[14] B. Müller, J. Reinhardt, M. T. Strickland, Neural Networks: an introduction (Berlin, 1995);
[15] W.J. Marciano, Phys. Rev. D29 (1984) 580.
[16] A. L. Deshpande, Nucl. Phys. Proc. Suppl. 105 (2002) 178.