

A determination of α_s from scaling violations using truncated moments

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Abstract

The strong coupling, $\alpha_s(M_Z)$, is determined from scaling violations of the nonsinglet DIS structure function, using 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.

Based on: S. Forte *et al.* : [hep-ph/0205286](https://arxiv.org/abs/hep-ph/0205286),
[hep-ph/0204232](https://arxiv.org/abs/hep-ph/0204232).

Outline of the method

- Our goal: a data-driven determination of α_s .
 - minimizing theoretical biases and uncertainties.
 - accurately assessing the effects of errors and correlations.
- Difficulties in extracting α_s from DIS data.
 - Mellin moments: a clean analytic NLO solution, however:
 - * Not directly measurable ($x \rightarrow 0$ implies $\sqrt{s} \rightarrow \infty$).
 - Momentum space evolution: no extrapolation, however:
 - * Integro-differential equation numerically more difficult.
 - * Parton parametrization necessary: theoretical bias, difficulties in assessing errors and propagating them to observables.
- Method: truncated moments.
 - Mellin moments over a truncated interval ($x_0 < x < 1$) are observable.
 - They obey a simple evolution equation approximated with arbitrary precision by a matrix equation.
 - In principle: a parametrization is not needed.
- Method: neural network parametrization of $F_2(x, Q^2)$.
 - In practice: data coverage and precision are not sufficient.
 - Neural networks: a bias-free parametrization of $F_2(x, Q^2)$.
 - All errors and correlations correctly taken into account.

Truncated moments of parton distributions

Truncated Mellin moments

$$q_n(x_0, t) \equiv \int_{x_0}^1 dx x^{n-1} q(x, t) .$$

satisfy the AP evolution equation ($t = \log \mu^2$)

$$\frac{d}{dt} q_n(x_0, t) = \frac{\alpha_s}{2\pi} \int_{x_0}^1 dy y^{n-1} q(y, t) G_n \left(\frac{x_0}{y}; \alpha_s \right) ,$$

where

$$G_n(x, \alpha_s) = \int_x^1 dz z^{n-1} P(z, \alpha_s) .$$

- As $x_0 \rightarrow 0$, G_n becomes the anomalous dimension γ_n . Different moments evolve independently.
- For $x_0 \neq 0$, evolution couples q_n with all q_k with $k > n$. To see it, Taylor expand $G_n(x_0/y)$ around $y = 1$.
- The Taylor expansion of G_n converges in $x_0 < y \leq 1$ (G_n only has integrable singularities due to $+$ distributions at $y = x_0$). Truncating it at the M -th term yields the linear system

$$\frac{d}{dt} q_n(x_0, t) = \frac{\alpha_s}{2\pi} \sum_{p=0}^M c_{p,n}^{(M)}(x_0, \alpha_s) q_{n+p}(x_0, t) .$$

Properties of truncated moments

- The matrix of anomalous dimensions governing the evolution of truncated moments is **upper triangular**.
 - Analytic diagonalization by recursion relation.
- Moments with significantly different indices are **weakly coupled** for small x_0 .
 - Legitimate truncation at finite M .
- The convergence of the series of approximations for increasing M can be **studied systematically**.
 - Study effects of remainder of AP *r.h.s.*
 - Evolve sample distributions with different methods.
- The convergence of the approximation as a function of M is good (few percent error for $M \lesssim 20$), **except for lowest nonsingular moments** (sensitive to singularities at $y = x_0$).
 - Improved version of the method is available
(see [A. Piccione, hep-ph/0107108](#))
 - For all finite moments $M \lesssim 12$ suffices.
- The method has been extended to **singlet and gluon** distributions, without new difficulties.
 - NLO analytic solution available in all cases.
 - Threshold logarithms can be included if appropriate.

Faithful parametrizations: problems

- **Standard procedure** for fitting PDF's and structure functions.
 - **Choose** a simple functional form with enough free parameters.
 - **Fix** parameters by minimizing χ^2 .
- **Difficulties** arise in determining errors on generic observables.
 - Errors and correlations of parameters require at least **fully correlated analysis of data errors**.
 - Error propagation to observables is **difficult/wrong**: many observables are nonlinear/nonlocal functionals of parameters.
 - **Theoretical bias** due to choice of parametrization is difficult to assess (effects can be large if data are not precise, *e.g.* with polarized distributions).
- **Goal**: a representation of the probability measure $\mathcal{P}(F_2)$ in the space of structure functions $F_2(x, Q^2)$. Then, for any functional $\mathcal{G}(F_2)$,

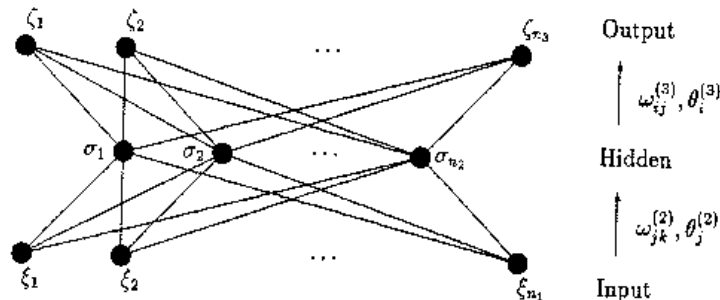
$$\langle \mathcal{G} [F_2(x, Q^2)] \rangle = \int \mathcal{D}F_2 \mathcal{G} [F_2(x, Q^2)] \mathcal{P}(F_2) ,$$

and similarly for higher moments.

- **Note**: a problem with a long history, active discussions in the context PDF global fits, different proposals available, see *e.g.* [hep-ph/0204316](#).

Neural networks: a solution

Neural networks are a class of algorithms providing robust, universal, unbiased approximants to incomplete or noisy data.



- **Building blocks:** neurons, *i.e.* input/output units characterized by activation

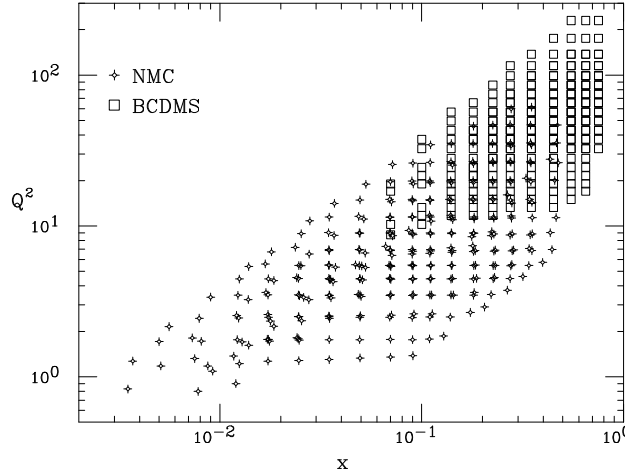
$$\xi_i = g \left(\sum_j \omega_{ij} \xi_j - \theta_i \right),$$

with (typically) $g(x) \equiv 1/(1 + \exp(-\beta x))$.

- **Parameters:** weights ω_{ij} , thresholds θ_i .
- **Architecture:** multilayer feed-forward NN. Each neuron receives input from neurons in preceding layer and feeds output to neurons in successive layer.
- **Learning:** supervised training by back-propagation. Network attempts matching data to output, weights and thresholds varied along steepest descent contours to minimize chosen error function.
- **Assumption:** smooth function. Size, architecture, learning cycle determined by statistical criteria.

Neural networks for structure functions

- **Data:** BCDMS and NMC: 552 data points for the nonsinglet structure function $F_2^{(NS)}(x, Q^2)$.



- **Method:** Monte Carlo + neural networks.
 - **Step 1** Generate an ensemble of N_{rep} pseudo-data sets, with the correct multivariate distribution given by experimental errors, fully correlated.

$$F_i^{(art)}(k) = (1 + r_{i,N}^{(k)} \sigma_{i,N}) \left[F_i^{(exp)} + \frac{\sum_a r_{i,a}^{(k)} f_{i,a}}{100} F_i^{(exp)} + r_{i,s} \sigma_{i,s} \right].$$

- **Step 2** Train N_{rep} neural networks, each one using one pseudo-data set.
- **Step 3** Evaluate averages, errors, correlations of observables using N_{rep} networks as Monte Carlo representation of probability measure in the space of structure functions.

Determination of α_S : choices

- Truncation point and fitting range.

Criteria:

- Data coverage \rightarrow small error on moments.
- High $Q^2 \rightarrow$ small power correction.
- Small x_0 , few intermediate scales \rightarrow small correlations between neighboring moments.

Choices: $x_0 = 0.03$; $20 \text{ GeV}^2 < Q^2 < 70 \text{ GeV}^2$; $n_{sc} = 3$.

- Evolution equation

- NLO evolution with matching at quark thresholds.
- Size: $M = 11$ with $n_{\min} = 1$.
- Auxiliary parameter for improved evolution: $N = 6$.
- \rightarrow Accuracy on evolution: 0.1%.

- Fitted moments

Criteria:

- Precision of fit requires $n_{\text{fit}} > 3$
- High correlations between neighboring moments may cause *off-diagonal instabilities* $\rightarrow n_{\text{fit}} < 6$.

Choices: Fitted moments: $n = 2, 4, 5, 6, 8$.

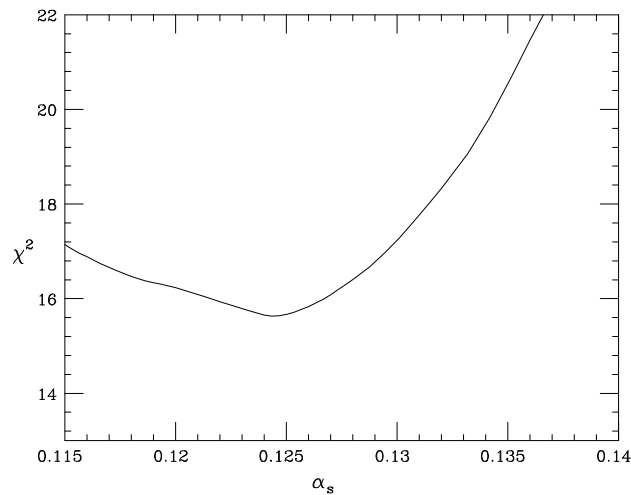
- Result with statistical error.

$$\alpha_S(M_Z) = 0.124 \pm_{-0.007}^{+0.004} \text{ (stat.) .}$$

Note: All fit parameters have been varied in the window of stability with negligible effects on the result.

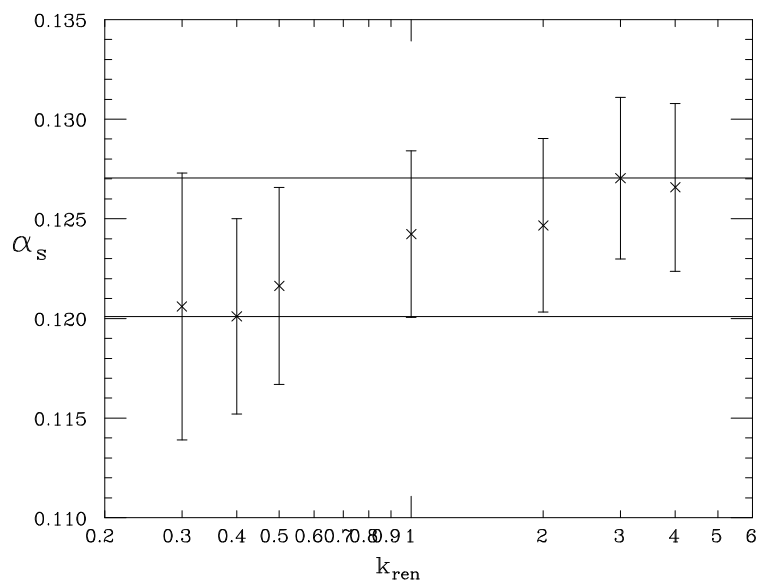
Determination of α_s : errors

- **Statistical error:** asymmetric χ^2 .

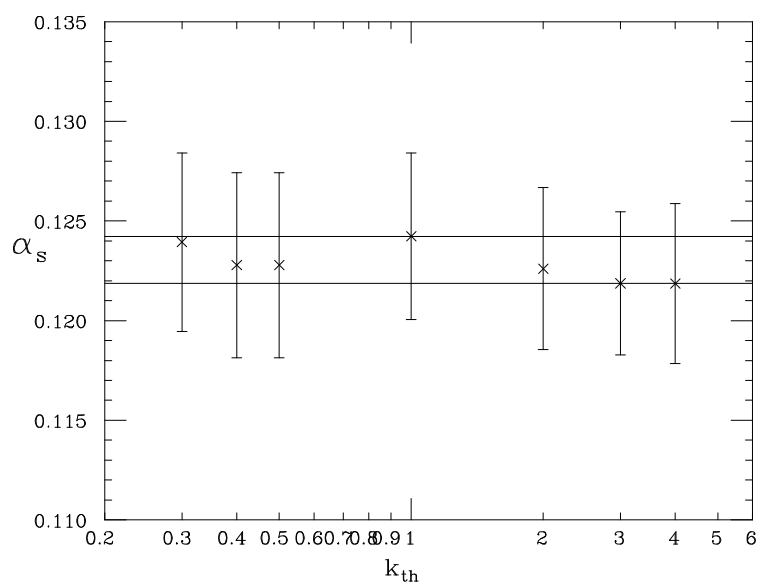


- **Theoretical error:** power correction.
Can be: **kinematical** (target mass corrections); **dynamical** (higher twist corrections); due to **elastic** contributions at $x = 1$. All are **negligible** ($< 1\%$) thanks to our choice of Q^2 range.
- **Theoretical error:** NNLO and higher perturbative evolution.
Estimated varying **renormalization scale** (no factorization mass dependence in DIS scheme), $\mu_{ren}^2 = k_{ren}Q^2$. **Not negligible**, indicating sizeable NNLO corrections. $\sigma_{ren} = \begin{matrix} + 0.003 \\ - 0.004 \end{matrix}$.
Note: possible enhancement of threshold logarithm effects.
- **Theoretical error:** Heavy quark thresholds.
Estimated varying the **threshold position** as $Q^2 = k_{th}M_q^2$. **Nearly negligible** in our Q^2 range (only b threshold included for some k_{th}). $\sigma_{th} = \begin{matrix} + 0.000 \\ - 0.002 \end{matrix}$.

- Varying the renormalization scale, $\mu_{ren}^2 = k_{ren} Q^2$.



- Varying threshold positions, $Q^2 = k_{th} M_q^2$.



- Our final result

$$\alpha_S(M_Z) = 0.124 \pm 0.004 \text{ (exp.)} \pm 0.003 \text{ (th.)} .$$

Summary

- We have determined the **strong coupling** $\alpha_S(M_Z)$ at NLO from **scaling violations** of NMC and BCDMS data for the nonsinglet DIS structure function, with the result

$$\alpha_S(M_Z) = 0.124 \begin{matrix} + 0.004 \\ - 0.007 \end{matrix} \text{ (exp.) } + \begin{matrix} 0.003 \\ - 0.004 \end{matrix} \text{ (th.) } .$$

- We have minimized theoretical biases and errors by using
 - **evolution with truncated moments**: minimize effects of parametrization by cutting out small x range; simple analytical expression for evolved distributions.
 - **parametrization with neural networks**: no theoretical bias, statistical control over accuracy of interpolation and extrapolation.
 - **choice of (x, Q^2) range** to minimize effects of nonperturbative and higher order corrections.
- **Statistical error** is significantly **larger** than theoretical one: improved data (especially deuteron), wider Q^2 range would significantly reduce errors.
- **Central value** is on **high side** of world average (though fully compatible); **error** is asymmetric.
- **NOTE: Threshold logarithms** $\log(Q^2(1-x))$ may affect our determination more significantly than others (see μ_{ren} dependence). They **can be** systematically **resummed** in Mellin space with truncated moments.