Drell-Yan transverse spectra at the LHC: a comparison of parton branching and analytical resummation approaches

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Abstract

I report on precision comparisons of theoretical predictions for Drell-Yan (DY) transverse momentum spectra from two approaches: the analytical resummation approach based on Collins-Soper-Sterman (CSS) formalism and the parton branching (PB) approach to the evolution of transverse momentum dependent (TMD) parton distributions.

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1 Introduction

Extensions of the QCD collinear factorization theorem [1] involving TMD parton distributions [2] are relevant to perform perturbative resummations to all orders in the strong coupling in kinematic regions of interest to collider physics, e.g. the Sudakov (or low-p_T) region [3–5] and high-energy (or low-x) region [6–8].

In the last few years, precision measurements of transverse momentum spectra in DY lepton-pair production have been carried out at the Large Hadron Collider (LHC) [9–12], which call for detailed studies of TMD resummations in the region of low vector-boson transverse momentum p_T.

In this article I report on a comparison of theoretical predictions for DY p_T spectra based on two different approaches: the analytical resummation approach based on the CSS formalism [3, 4] and the PB approach [13, 14] to the evolution of TMD distributions. I start in Sec. 2 by briefly recalling the basic elements of the two methods. In Sec. 3 I compare them at analytical level. In Sec. 4 I present numerical comparisons. I give conclusions in Sec. 5.

2 Theoretical methods

2.1 CSS method

The CSS method [3, 4] decomposes the DY differential cross section into the sum of the resummed term (dominant for $p_T \ll Q$, where Q is the vector boson invariant mass) and the finite term (important for p_T of order Q). The resummed term is factorized in impact parameter space into a hard-scattering coefficient function and TMD distributions, which in turn are expressed as convolutions of Sudakov form factors, collinear evolution coefficients and parton distributions.

The resummed and finite terms require an appropriate *matching* procedure in order to avoid double counting. The matching can be done by subtracting counterterms from the resummed cross section [15–17].

Nonperturbative effects are incorporated in the formalism through a Gaussian smearing factor in impact parameter space, as well as nonperturbative contributions to Sudakov evolution [18–21].

2.2 PB method

The parton branching (PB) method [13, 14] formulates the evolution of TMD distributions in terms of Sudakov form factors and real emission splitting functions using the *unitarity* picture of parton interactions commonly employed in showering Monte Carlo algorithms [22,23]. The resolvable and non-resolvable regions of the branching phase space are separated by the soft-gluon resolution scale z_M (in general, branching scale dependent [24]). Soft-gluon angular ordering is implemented in the TMD evolution so that color coherence effects are taken into account and the collinear limit agrees with the coherent branching approach of Refs. [23, 25].

The matching with finite-order hard-scattering matrix elements is not done additively as in the CSS framework, but rather by using the showering operator method with subtracted matrix elements [26–28].

Nonperturbative TMD effects are encaptured in the TMD distribution at the starting evolution scale $\mu_0 = \mathcal{O}(1 \text{ GeV})$, which is parametrized (for instance, as a transverse momentum Gaussian times a longitudinal momentum distribution in a simplest parametrization) and determined from fits to experimental data [29].

3 Analytical comparison

The Sudakov form factor in CSS is written as

$$S(Q,b) = \exp\left(-\int_{b_0/b^2}^{Q^2} \frac{d\mu^2}{\mu^2}\left[\ln\left(\frac{Q^2}{\mu^2}\right)A(\alpha_s(\mu^2)) + B(\alpha_s(\mu^2))\right]\right), \tag{1}$$

where b is the impact parameter, and the functions A and B are perturbatively calculable as power series expansions in α_s, $A = \sum_n A^{(n)}\alpha_s^n$, $B = \sum_n B^{(n)}\alpha_s^n$, and control the resummation of double-logarithmic and single-logarithmic perturbative corrections respectively, with $A^{(1)}$ corresponding to leading logarithms (LL), $A^{(2)}$ and $B^{(1)}$ corresponding to next-to-leading logarithms (NLL), and so on.

The Sudakov form factor in PB is written as

$$\Delta_a(\mu^2,\mu_0^2) = \exp\left(-\sum_b \int_{\mu_0^2}^{\mu^2} \frac{d\mu'^2}{\mu'^2} \int_0^{z_M} dz\; z\, P_{ba}^{(R)}(\alpha_s(q_t),z)\right), \tag{2}$$

where z_M is the soft-gluon resolution scale and $P_{ba}^{(R)}$ are the real emission splitting functions, perturbatively calculable as power series expansions in α_s. By rewriting the PB Sudakov using the momentum sum rule, virtual splitting functions and the angular ordering condition, we can compare the CSS perturbative coefficients $A^{(i)}$ with the PB coefficients $k^{(i-1)}$ of Ref. [13], and the CSS perturbative coefficients $B^{(i)}$ with the PB coefficients $d^{(i-1)}$ of Ref. [13].

At LL and NLL level, all coefficients are in agreement between CSS and PB [30]. At next-to-next-to-leading logarithms (NNLL), differences between coefficients both at the single and double logarithmic level are observed which can be understood [30] either as a result of renormalization group transformations and resummation scheme dependence [15,16] (in the single-log coefficients) or as an effect of soft-gluon effective coupling [31–33] (in the double-log coefficients). This gives the possibility of future systematic comparisons of precision predictions in the phase space regions influenced by Sudakov resummation.

4 Numerical comparison

First numerical comparisons have been performed for the DY transverse momentum spectrum based on the implementation of the CSS method in the reSolve [34] event generator and on the implementation of the PB method in the Cascade [35,36] event generator, supplemented by the uPDFevolv program [37] for TMD evolution.

reSolve implements the resummed part of the cross section as described by CSS up to NNLL accuracy [34,38]. Matching of the resummed part to finite-order terms is not included. The result for the p_T spectrum is shown in the left plot of Fig. 1.

The calculation with Cascade implements the PB TMD, and performs the matching with NLO hard-scattering events from Madgraph_aMC@NLO [39], in combination with the TMD. For this calculation the PB-NLO-HERAI+II-2018-set2 TMD PDF [29] is extracted from TMDlib [40,41] and used by Cascade. The matching of the NLO events to the TMD evolution is done as in Ref. [28] by using Herwig6 subtraction terms [42] and a matching scale to avoid double counting. The result with PB is shown in the right plot of Fig. 1.

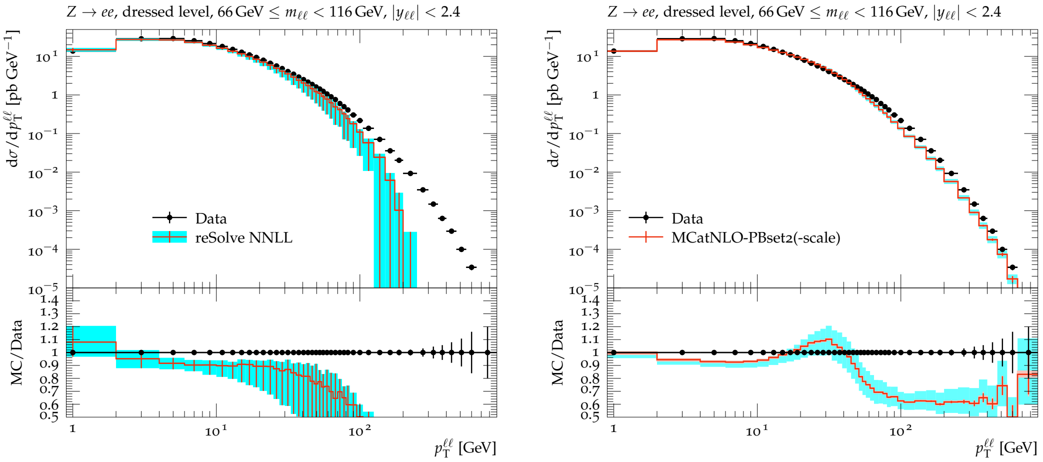

Figure 1: Inclusive Z boson p_T spectrum by reSolve/CSS (left) and Cascade/PB (right). Theoretical uncertainty bands are shown in blue.

From the plots, a few observations can be made. Firstly, both approaches have an accurate prediction in the low-p_T region up to $p_T \sim 20$ GeV. The predictions fail to describe the high-p_T region for different reasons. In reSolve it is due to absence of finite-order terms. The PB TMD is matched to NLO hard-scattering events for inclusive Z production. The deficit at high-p_T is due to missing higher orders or higher jet multiplicities. One way to increase accuracy for the high-p_T tail is to include TMD *merging* with higher jet multiplicities, as in Ref. [43].

The second observation is that the theory uncertainties are calculated differently. In RESOLVE they are obtained by varying three scales: the renormalization (μ_R), factorization (μ_F) and resummation (μ_S) scales. Since the resummation scale is mostly important for matching to finite terms, the variation of μ_S gives a distorted view of the uncertainty at the intermediate p_T region. The PB uncertainties in Fig. 1 include only two scale variations, that of μ_R and μ_F. The matching scale has not been varied yet. Besides these uncertainties, there are also TMD uncertainties. In this kinematic range of energy, mass and transverse momentum, these are much smaller than the scale variations.

Finally, the nonperturbative contributions are different. In the CSS implementation of reSolve, the nonperturbative factor is an overall Gaussian smearing factor of the form $\exp(-g b^2)$ [34]. In PB, the starting TMD contains all the nonperturbative parts. The intrinsic transverse momentum (e.g. a Gaussian $\exp(-k_T^2/2\sigma^2)$) gets smeared out by the TMD evolution [28,29].

5 Conclusion

Two formalisms that include TMD physics, CSS and PB, have been systematically compared with respect to Sudakov resummation for DY p_T spectra. At analytical level, CSS and PB coincide at LL and NLL order and differences at higher order coefficients are being tracked down. Numerically, both approaches are describing the low-p_T region of the DY p_T spectrum. Differences are observed in the estimation of theory uncertainties and the parametrization of nonperturbative effects. The features that emerged are potentially important for high-precision DY phenomenology and are well-suited within benchmark exercises for the LHC and future colliders.

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