

Heavy Quarks in PDF's fits for pedestrians (myself included)

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First of all, an assumption:

We all agree on the partons

i.e. purely massless $\overline{\text{MS}}$, evolved through the heavy quark thresholds with variable flavour number

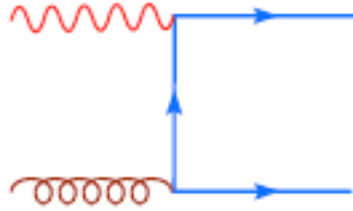
If we do (do we?), then the issue is
how to calculate the cross sections

[Normally a user issue, but the fitters also have to deal with it]

Possible approaches for F_2

FFN

$$F_2^h \sim \sum_{\text{light partons}} f_i(\mu) \otimes C_i^{\overline{MS}}(Q, m, \mu)$$



Proper m/Q mass terms

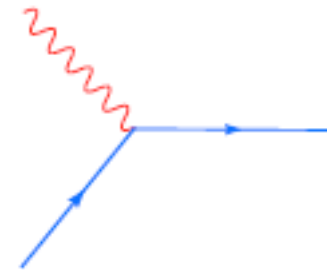
Unresummed $\log(Q/m)$ term



Fails in $Q \gg m$ limit

ZM (resummed)

$$F_2^h \sim \sum_{\text{all partons}} f_i(\mu) \otimes C_i^{\overline{MS}}(Q, \mu)$$



Resummed $\log(Q/m)$ terms

Missing m/Q terms



Fails in $Q \sim m$ threshold region

Matching

An obvious solution would seem to be

$$F_2 = \text{FFN} + \text{ZM} - \text{subtraction}$$

where

$$\text{subtraction} = \left\{ \begin{array}{l} O(\alpha_s^n) \text{ limit of ZM} \\ \text{quasi-collinear limit of FFN} \end{array} \right.$$

Everybody does something like this

Matching

In an ideal world the matching would be smooth

$$F_2 = \text{FFN} + \text{ZM} - \text{subtraction}$$


At $Q \sim m$ these two cancel,
leaving only the FFN

At large Q these two terms cancel,
leaving the resummed ZM one

However, the devil lies in the details

The devil

$$F_2 = \text{FFN} + \text{ZM} - \text{subtraction}$$


This terms starts one order higher than FFN.

A priori, it **does not** contain the correct mass effects

Its naive behaviour is usually unphysical: need a prescription
(Doing nothing is formally qualitatively equivalent to choosing a prescription, but it can make an important quantitative difference)

How to include such mass effects, which are **not known** from an explicit calculation, is precisely the source of the ambiguity between different approaches

Some food for thought

Cross section predictions are intrinsically **ambiguous** in the threshold region

- Can we agree on a prescription?
- Should we actually agree on one?
Won't the artificial agreement hide the uncertainty?
- Can we quantify the size of the ambiguity?
Does it actually matter given the size of the experimental errors?
Will it matter in the future?

Some food for thought

Assuming that the ambiguity does matter numerically then

- Should we fit in the threshold regions, knowing that the resulting partons will be prescription-dependent?
- Does it make sense to skip these regions altogether? Would we be throwing away too many data points?

Answers (hopefully) from the following talks and the discussion