

# Dynamic Alignment Method at the LHC

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## Abstract

The dynamic alignment method of the forward proton detectors proposed by the CDF Collaboration is reviewed. Applicability of the method at the LHC is discussed.

## 1 Introduction

A typical  $pp$  collision at the LHC consists of several parton-parton interactions. This causes the color charge flow between the protons and leads to color dipoles creation. In consequence, the dipoles radiate filling the detector with particles. However, in a fraction of events the protons interact coherently, either electromagnetically – exchanging a photon, or strongly – via an exchange of a color singlet object named Pomeron. In such collision one or both protons, staying intact, may lose some part of their energy and be scattered at very small angles into the accelerator beam pipe. Since the exchanged object is a color singlet, a suppression of particle radiation is observed in such events. This leads to a presence of rapidity regions devoid of particles – the rapidity gaps.

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When both protons stay intact and two emitted photons or Pomerons interact with each other producing a state in the central part of the rapidity space, the event is called a Central Exclusive Production (CEP) [1]. Various objects can be produced in such a process: particles ( $\chi_c$ , Higgs boson,  $J/\psi$ ) or systems of particles (these may be a pair of leptons, photons, jets, SUSY particles, *etc.*). At hadron colliders such processes give a unique opportunity to measure all final state particles, which leads to kinematic constraints and results in a good resolution of the centrally produced system mass reconstruction in a wide range of masses [2]. This can be done with proton tagging detectors that are inserted into the beam pipe far away from the Interaction Point (typically several dozens or even hundreds of metres).

At the LHC, both ATLAS and CMS Collaborations are equipped with such detectors – ALFA (Absolute Luminosity For ATLAS) and TOTEM (Total Cross Section, Elastic Scattering and Diffraction Dissociation), respectively. However, both detector systems are designed to work during dedicated LHC runs with special machine tune (the so-called high  $\beta^*$  optics), when the luminosity is a few orders of magnitude smaller than the nominal  $10^{34} \text{ cm}^{-2} \text{ s}^{-1}$ . Therefore, both Collaborations plan to install additional detectors that will be able to work in the standard LHC tune environment: the AFP (ATLAS Forward Physics) detectors and the HPS (High Precision Spectrometer) for ATLAS and CMS respectively.

Forward proton detectors can measure the position and direction of the scattered proton trajectory. From that measurement, the fractional momentum loss,  $\xi = (E_0 - E')/E_0$ , and the four-momentum transfer,  $t \approx p_T^2 = p_x^2 + p_y^2$ , can be reconstructed (actually, the value of four-momentum transfer is negative and  $t$  denotes hereafter its absolute value). A crucial element for the reconstruction resolution is proper alignment of detectors, *i.e.* a precise knowledge of their position. One should note that detectors position (their distance from the beam) has to be adjusted according to the actual beam conditions – the detectors must be movable. For instance, at early stages of a run, when the beam is not very stable, the detectors are situated in their home positions. Later, they are inserted into the beam pipe and placed in the immediate vicinity of the beam. As the detectors positions need to be established on the run-by-run basis, one needs a data-driven method of aligning forward proton detectors.

## 2 Dynamic Alignment Method

The dynamic alignment method [3, 4] has been used by CDF for their RPS (Roman Pot Spectrometer) detector. For a given time period a sample of single diffractive events was collected. Then four-momentum transfer distribution was reconstructed assuming different detectors positions. In particular, one is interested in the distribution value at  $t' = 0$  (in the following, primed variables denote the reconstructed values and unprimed variables are used for the true

values of observables):

$$S = \left. \frac{d\sigma}{dt'} \right|_{t'=0}.$$

When the assumed detectors positions are wrong, such is also the value of the reconstructed four-momentum transfer. Thus,  $S$  is a function of the misalignment. The dynamic alignment method assumes that  $S$  reaches a maximum value for the perfectly aligned detectors. In the following a simplified justification of this method is given.

As mentioned before, the detectors measure trajectories of scattered particles, *i.e.* the trajectory position  $(x, y)$  and its elevation angles (slopes)  $(s_x, s_y)$ . In the simplest case there are two detector stations per beam, both measuring proton position:  $(x_1, y_1)$  at  $z_1$  and  $(x_2, y_2)$  at  $z_2$ , spaced by the distance  $L = z_2 - z_1$ . The parameters of the trajectory at the mid point,  $z = (z_1 + z_2)/2$ , are:

$$x = \frac{x_1 + x_2}{2}, \quad y = \frac{y_1 + y_2}{2}, \quad s_x = \frac{x_2 - x_1}{L}, \quad s_y = \frac{y_2 - y_1}{L}.$$

The misalignment of such detectors has four degrees of freedom, for both stations and both directions:  $\Delta x_1, \Delta y_1, \Delta x_2, \Delta y_2$ . In fact, one should include also possible misalignment of the  $z$  detector position and skewness of the coordinate system, but in a real experimental environment they are negligible. It will prove to be helpful to use the global:

$$\Delta x = \frac{\Delta x_1 + \Delta x_2}{2}, \quad \Delta y = \frac{\Delta y_1 + \Delta y_2}{2},$$

and the relative:

$$\delta x = \Delta x_2 - \Delta x_1, \quad \delta y = \Delta y_2 - \Delta y_1,$$

misalignments, instead of  $\Delta x_1, \Delta y_1, \Delta x_2, \Delta y_2$ .

A large fraction of protons tagged in forward detectors originate from single diffractive processes (*i.e.* single diffractive dissociation). The four-momentum transfer distribution of these events is exponential:

$$\frac{d\sigma}{dt} = \sigma_0 b e^{-bt},$$

here  $\sigma_0$  is the single diffraction cross section and  $b$  is the nuclear slope. When a proton is tagged, its initial momentum (momentum at the Interaction Point, IP) is unfolded from the measured values of  $(x, y, s_x, s_y)$ . In particular:

$$p_x = f(x, y, s_x, s_y), \quad p_y = g(x, y, s_x, s_y).$$

Afterwards these values are used to calculate the four-momentum transfer. However, if the detectors are misaligned, the unfolded momentum differs from the real one:

$$p'_x = p_x + \Delta x, \quad p'_y = p_y + \Delta y,$$

where:

$$\begin{aligned}\Delta_x &\approx \frac{\partial f}{\partial x} \Delta x + \frac{\partial f}{\partial y} \Delta y + \frac{\partial f}{\partial s_x} \frac{\delta x}{L} + \frac{\partial f}{\partial s_y} \frac{\delta y}{L}, \\ \Delta_y &\approx \frac{\partial g}{\partial x} \Delta x + \frac{\partial g}{\partial y} \Delta y + \frac{\partial g}{\partial s_x} \frac{\delta x}{L} + \frac{\partial g}{\partial s_y} \frac{\delta y}{L}.\end{aligned}$$

As  $t \approx p_x^2 + p_y^2$  and  $t' \approx (p'_x)^2 + (p'_y)^2$ , one can obtain the reconstructed four-momentum transfer distribution (assuming that  $\Delta_x$  and  $\Delta_y$  are proton momentum independent):

$$\frac{d\sigma}{dt' d\varphi'} = \frac{\sigma_0 b}{2\pi} e^{-b(t' - 2\sqrt{t'} \Delta \cos(\varphi' - \alpha) + \Delta^2)},$$

where  $\Delta$ ,  $\varphi'$  and  $\alpha$  are defined by:

$$p'_x = \sqrt{t'} \cos \varphi', \quad p'_y = \sqrt{t'} \sin \varphi', \quad \Delta_x = \Delta \cos \alpha, \quad \Delta_y = \Delta \sin \alpha.$$

Expanding  $\exp(2b\sqrt{t'} \Delta \cos(\varphi' - \alpha))$  into a power series one obtains:

$$S = \left. \frac{d\sigma}{dt'} \right|_{t'=0} = \sigma_0 b e^{-b\Delta^2}.$$

This shows that for perfect alignment  $S$  indeed reaches its maximal value.

At this point there some important remarks are to be made. Firstly, to be able to reconstruct the  $t$  distribution at  $t = 0$ , such events must be within the acceptance of the detector. As will be discussed later on it is not always the case.

Secondly, the derivation presented above assumes that  $\Delta_x$  and  $\Delta_y$  are constant (not depending on the proton momentum), *i.e.* higher derivatives of  $f$  and  $g$  are zero. This assumption is needed only to obtain the analytic formula for  $S$ , but is not crucial for the method. However, there are restrictions on the possible variation of  $\Delta_x$  and  $\Delta_y$  – on the average they must be substantially different from zero, otherwise the net effect cancels.

Thirdly, the fact that for the perfect alignment  $S$  gets maximal does not mean that by maximisation of  $S$  one aligns the detectors. This is because maximising  $S$  is equivalent to requesting  $\Delta_x = 0$  and  $\Delta_y = 0$ . These two equations do not have a unique solution, as there are four unknown misalignments. However, when the matrix of partial derivatives of  $f$  and  $g$ :

$$\begin{pmatrix} \partial_x f & \partial_x g \\ \partial_y f & \partial_y g \\ \partial_{s_x} f & \partial_{s_x} g \\ \partial_{s_y} f & \partial_{s_y} g \end{pmatrix}$$

has two rows that are negligible and the remaining two rows form a matrix with non-vanishing determinant, the method provides a direct alignment for variables corresponding to non-negligible rows. Otherwise one needs another method that will give the two missing constraints.

Finally, one must remember that there are additional experimental effects that influence the measurement. Such factors (*e.g.* spatial resolution of the detectors, beam angular spread) cause random smearing of the reconstructed four-momentum transfer leading to statistical errors of the obtained  $t$  distribution. Thus, for a given number of collected single diffractive events there is a limit on the alignment precision.

### 3 Alignment at the LHC

In this section the dynamic alignment method applicability at the LHC is presented; the forward proton detectors in the ATLAS experiments are considered – the ALFA [5] and the AFP detectors at 220 m (AFP220) [6].

The ALFA detector stations consist of two roman pots at each outgoing beam, positioned symmetrically with respect to the IP at 237.4 and 241.5 metres. Each pot allows to insert vertically the position sensitive and triggering detectors into the beam pipe. The detectors will use the scintillating fibers to measure the scattered proton position.

The main purpose of ALFA is to measure the elastic proton-proton scattering in the Coulomb amplitude dominance region. This allows for precise calculations of the scattering amplitude and hence precise determination of the luminosity. As already mentioned, for that purpose a special high  $\beta^*$  optics will be used. This causes that single diffractive events with  $t = 0$  are not within the detectors acceptance, for all possible proton momentum losses [7]. Therefore, the dynamic alignment method cannot be used for the ALFA detectors.

The AFP220 detectors are currently at the R&D stage and are planned for installation during the LHC shutdown before the  $10^{34} \text{ cm}^{-2} \text{ s}^{-1}$  luminosity runs (however, possibilities of earlier installation are also discussed).

Like for the ALFA experiment, two detector stations per an outgoing beam are planned – they will be positioned symmetrically at 226 and 224 metres away from the ATLAS IP. However, instead of roman pots, the Hamburg movable beam pipe mechanism [8, 9] will be used to insert the detectors inside the beam pipe. Each station will consist of a silicon detector, for the proton position measurement, and a fast timing detector (with resolution of several picoseconds) that is necessary for the pile-up background reduction.

As discussed in Section 2, crucial for the method are the derivatives of the  $p_x$  and  $p_y$  unfolding functions ( $f$  and  $g$ ) with respect to  $x$ ,  $y$ ,  $s_x$  and  $s_y$ . Ranges of the derivatives for the AFP220 case are given in Table 1. These were calculated for single diffractive events generated with Pythia 6.4 [11], transported with FPTrack [12] and then unfolded as in [2].

It can be seen that in the first column the most significant element is the  $\partial_{s_x}$  and for the second column the most important is the  $\partial_{s_y}$ . Therefore, for

Table 1: Approximate ranges of  $f(x, y, x', y')$  and  $g(x, y, x', y')$  derivatives for the standard LHC tune (V6.5, collision [10]).

	$f(x, y, x', y')$	$g(x, y, x', y')$
$\partial_x$	$(-2 \pm 4) \cdot 10^1$	$(-1 \pm 1) \cdot 10^2$
$\partial_y$	0	0
$\frac{1}{L}\partial_{sx}$	$(2.5 \pm 1) \cdot 10^3$	$(4 \pm 2.5) \cdot 10^2$
$\frac{1}{L}\partial_{sy}$	0	$(-3 \pm 2) \cdot 10^3$

both columns, the  $\partial_x$  and  $\partial_y$  rows can be neglected. The remaining  $\partial_{sx}$  and  $\partial_{sy}$  rows form a matrix with non-zero determinant, which depends only on the most significant elements in each column. This shows that the dynamic alignment method will work for the AFP220 detectors. However, in contrast to the situation of the CDF detectors, the method is sensitive to the relative alignment and not to the global one.

This is illustrated in Figures 1 and 2, where the reconstructed four-momentum transfer distributions are presented for different values of  $\delta x$  and  $\delta y$ :  $0 \mu\text{m}$ ,  $\pm 30 \mu\text{m}$  and  $\pm 50 \mu\text{m}$ . Indeed, the simulation, which includes the spatial resolution and the multiple Coulomb scattering at the station at 216 metres [2], confirms the conclusions that were obtained from the analysis of the  $f$  and  $g$  derivatives. The four-momentum transfer distribution at  $t = 0$  decreases when relative misalignment is introduced. Such behaviour is not observed in case of the global misalignment. This follows from the fact that  $\partial_x$  and  $\partial_y$  columns in Table 1 are practically negligible. Also, as can be seen from Figures 1 and 2, the sensitivity to the relative misalignment in the vertical direction is smaller than that for the horizontal one.

## 4 Conclusions

The dynamic alignment method for the forward proton tagging detectors proposed by the CDF Collaboration was reviewed. A simplified mathematical justification of this method was given and its applicability at the LHC was discussed. It was shown that it works there differently than at the Tevaron, where it enabled to determine the global alignment of the CDF RPS detectors. In the ATLAS Experiment the method it is not useful for the ALFA detectors, whereas it can be successfully employed for relative alignment of the AFP220 stations.

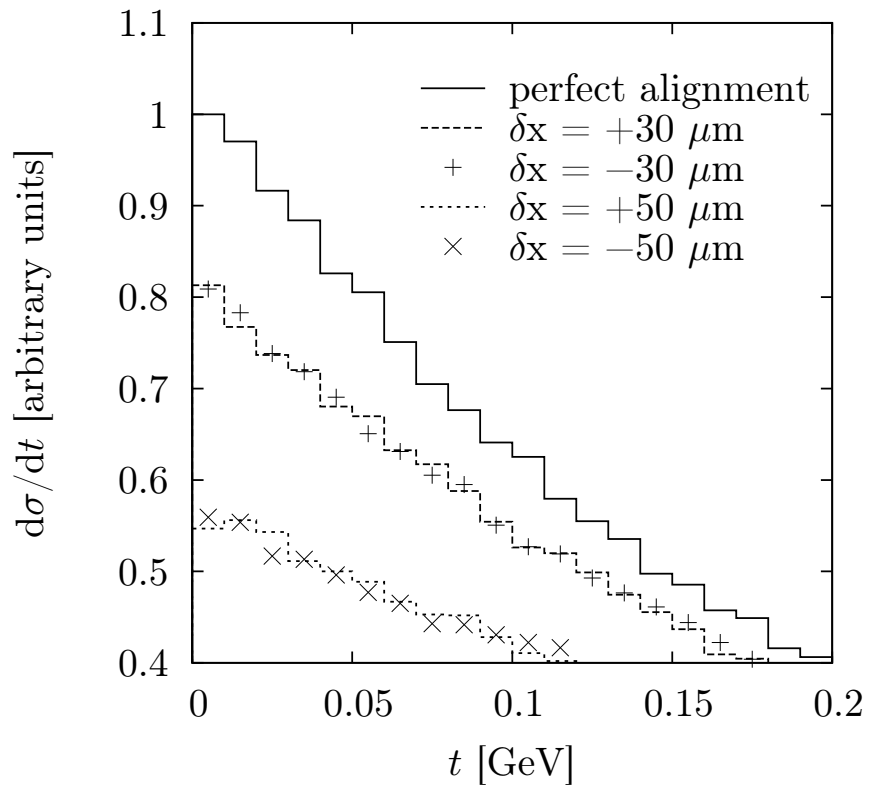


Figure 1: Reconstructed four-momentum distribution for different values of horizontal misalignment ( $\delta x$ ).

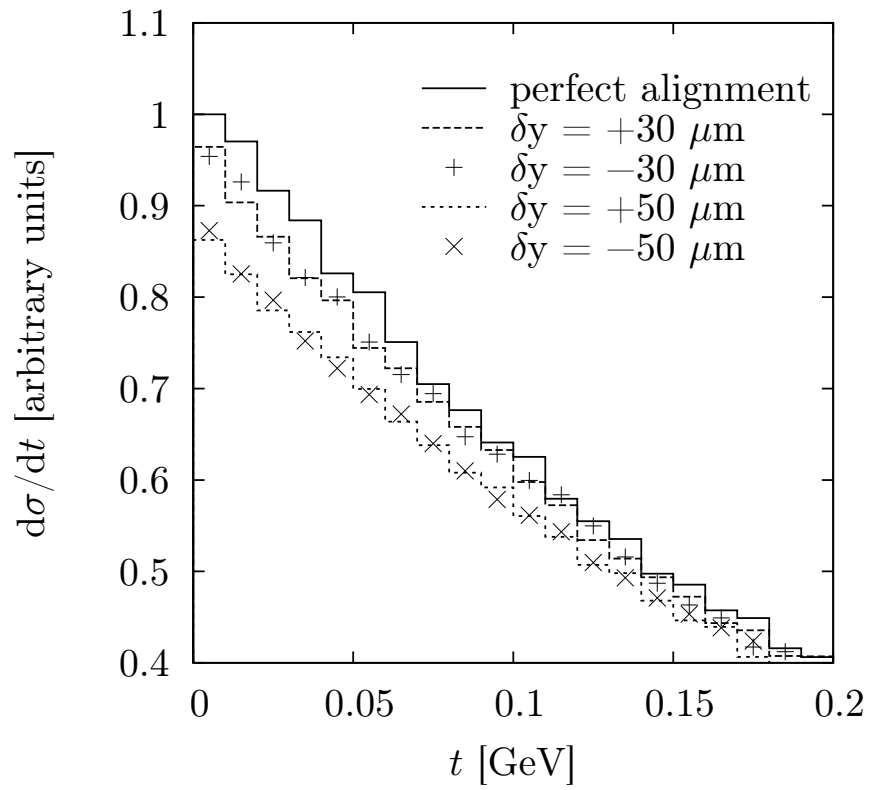


Figure 2: Reconstructed four-momentum distribution for different values of vertical misalignment ( $\delta y$ ).



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