

HOT-SPOT METHOD FOR ALIGNMENT OF FORWARD PROTON DETECTORS AT THE LHC*

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(Received April 11, 2016)

A method for alignment of the forward proton detectors at the LHC based on the characteristic shape of the hit pattern containing a dense region is presented. The precision of the method is discussed, including the systematic uncertainties.

DOI:10.5506/APhysPolB.47.1619

1. Introduction

One of the elements of the physics programme of the Large Hadron Collider (LHC) experiments are the measurements of diffractive processes. These processes are a result of a colour singlet exchange between the interacting protons. One of the distinctive experimental signatures of diffractive processes is the presence of an intact forward proton in the final state. Diffractive protons are scattered at very small angles (into the accelerator beam pipe) and can be registered only by using dedicated detectors. Such detectors need to be placed in a close proximity to the proton beam and far away from the interaction point.

Presently, several proton tagging detectors are installed at the LHC, namely: TOTEM [1], ALFA [2] and AFP [3]. The main goal of ALFA (Absolute Luminosity for ATLAS) is to detect the elastic scattering events, in

* Presented at the Cracow Epiphany Conference on the Physics in LHC Run 2, Kraków, Poland, January 7–9, 2016.

order to measure the elastic t -spectrum and to determine the total cross section (via the optical theorem), and the absolute luminosity (via the Coulomb interactions). The AFP (ATLAS Forward Proton) detectors aim at the detection of diffractively, but inelastically, scattered proton. The TOTEM experiment, including its recent addition — the CMS-TOTEM Precision Proton Spectrometer (CT-PPS) [4], has similar goals as ALFA and AFP, but performs the measurements in a different interaction point¹.

The following study was performed for the AFP detectors. However, the presented methods are not based on the design of a particular detector, but rather on the properties of the accelerator optics. Therefore, they have potentially wider applications than only the alignment of the AFP detectors.

The AFP is foreseen to consist of four stations, two on each side of the ATLAS interaction point, at 205 and 217 meters away. Each station will contain four planes of silicon pixel detectors, providing the overall resolution of 10 μm in the horizontal direction and 30 μm in the vertical direction. In addition, in the outer (217 m) stations, the time-of-flight detectors with a 30 ps resolution will be located. The AFP detectors will be placed in the Roman Pots to allow their movement with respect to the LHC beam.

The aim of the alignment procedure is to find an exact position of a detector. This is particularly important for the AFP detectors, since they are inserted and retracted for each data-taking period, so each time their position can be different. Precise knowledge of the detector position is a must for a reliable comparison of the data collected during different periods and for the reconstruction of the scattered proton kinematics [5]. Therefore, dedicated, preferably data-driven, alignment methods are essential for the data quality and for minimizing the uncertainties of the final measurements.

2. The hot-spot method

Figure 1 presents the distribution of the proton transverse position at 205 meters from the ATLAS interaction point. It was obtained using PYTHIA 8 [6] generated single diffractive events at $\sqrt{s} = 14$ TeV. The protons were transported through the LHC magnetic lattice using the MAD-X programme [7] with $\beta^* = 0.55$ m optics settings. The distinctive pattern seen in the plot, in particular the presence of a narrow region — the hot spot, is an effect of the LHC optics properties and the kinematic distribution of diffractive protons.

The principle of the hot-spot method is to use the narrow region seen in the transverse hit pattern as the reference point. The position of the hot spot is known from the simulation and it can be measured in the data. The comparison of these two positions give information about the position of the detector during the data taking.

¹ The LHC beams interact in four places.

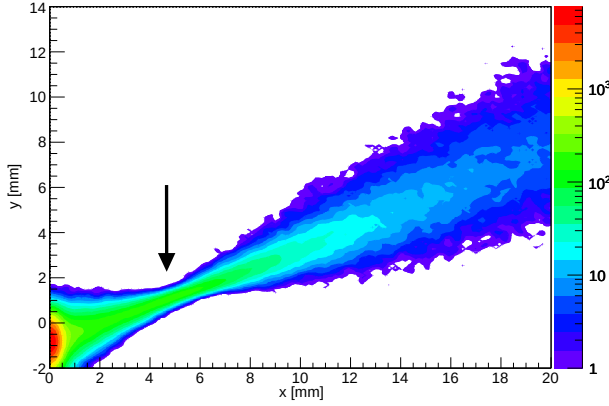


Fig. 1. Distribution of simulated transverse proton positions transported with MAD-X [7] through the LHC magnet lattice to the detector plane. The hot spot is marked with the arrow.

The hot-spot method has several advantages. It provides the alignment information individually for each detector, independently of the others. This is in contrast to other methods [3], which rely on information from several detectors. In addition, since the hot-spot method uses the hit pattern of single diffractive protons, the large cross section for this process results in a high statistics that can be used in the alignment analysis.

The hot-spot position is found in the following way. The two-dimensional distribution is divided into vertical slices (divisions along x axis). For each slice, the width of the distribution in y is determined and then plotted as a function of x . The obtained dependence shows a clear minimum defining the hot spot, see Fig. 2. To find its position, a second order polynomial fit is performed.

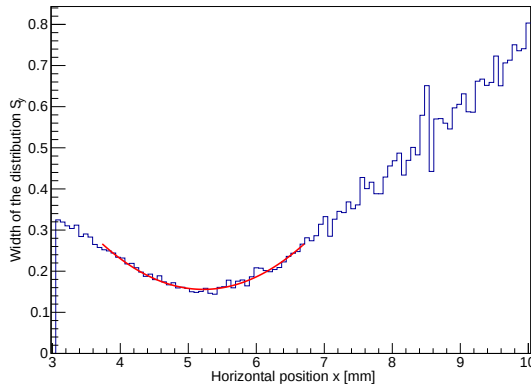


Fig. 2. Vertical width of the hit pattern as a function of the horizontal coordinate.

3. Alignment precision

The resulting position of the hot spot depends on the details of the analysis. This leads to systematic uncertainties of the method and will be discussed in the following.

The element that affects the results the most is the method used to calculate the y -distribution width. Here, two methods were considered: the standard deviation and the width of a Gaussian fit. The hot-spot positions found with these two methods differ by about $200\ \mu\text{m}$. This large difference is a result of the non-Gaussian shape of the y -distribution. Figure 3 presents an example of this distribution, together with the Gaussian fit, for one of the slices close to the hot spot.

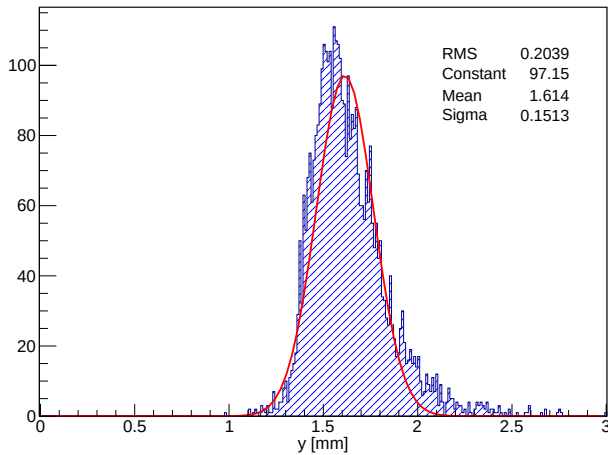


Fig. 3. (Colour on-line) Vertical proton position distribution in a proximity to the hot spot. A Gaussian fit is plotted with a black/red line.

One should note that since the standard deviation and the Gaussian width are sensitive to slightly different properties of the distribution, they actually *define* the hot-spot position differently. However, a similar situation will occur also when the algorithms are applied to the data. Therefore, the value of $200\ \mu\text{m}$ does not reflect the uncertainty, but only quantify the difference between the two definitions. In reality, the uncertainty for the data can be determined by comparing the detector positions obtained with the two methods.

The next source of uncertainty is related to the choice of the binning. The method using the standard deviation depends on the size of the x -slices, and the estimated uncertainty was $40\ \mu\text{m}$. The method using the Gaussian fit depends also on the y -bin size. Here, the uncertainty was found to be $28\ \mu\text{m}$.

Another parameter of the procedure is the range in which the polynomial fit is performed. For the standard deviation, the corresponding uncertainty is $30\ \mu\text{m}$ and $25\ \mu\text{m}$ for the Gaussian fit.

The last systematic effect studied in this analysis was the influence of the physics model and background. As already mentioned, the hit pattern presented in Fig. 1 depends on the assumptions for the kinematic distribution of diffractive protons. Also, the beam-related background, which is not taken into account in the simulations, can affect the reconstructed position of the hot spot. In order to estimate the size of these effects, two samples were compared. The first one consisted of protons originating from single diffractive processes, while the other one had an admixture of protons coming from double diffractive events.

The difference between the determined hot-spot positions reflects the sensitivity of the alignment to the physics model and the background. The method using the Gaussian fit results in the uncertainty of $8\ \mu\text{m}$, which is smaller than $26\ \mu\text{m}$ obtained with the standard deviation method.

It must be pointed out that the above results were obtained using the samples of 5×10^6 diffractive protons. This corresponds to the integrated luminosity of about $200\ \mu\text{b}^{-1}$, a relatively small value at the LHC. In reality, one can expect much greater luminosity². It is possible that with the increased statistics, some of the uncertainties discussed above will decrease, in particular the ones related to the size of the bins.

In addition, one has to take into account the uncertainty resulting from statistical fluctuations of a finite sample. To quantify this effect, the alignment procedure was applied to many statistically equivalent, but independent samples created using the bootstrap technique. The spread of the obtained positions reflects the statistical uncertainty, which is equal to $30\ \mu\text{m}$ and $18\ \mu\text{m}$ for the standard deviation and the Gaussian width methods, respectively.

4. Summary and conclusions

The hot-spot method of the alignment uses the characteristic proton hit pattern observed in the AFP detectors. It can be applied independently to each detector. The method uses the protons originating from the single diffractive dissociation processes, which leads to large statistics. Therefore, the alignment can be performed even for relatively short periods of time.

² The number of registered events depends on distance between the detectors and the beam. However, only the events in the vicinity of the hot spot are important, not the total number. Therefore, a good variable to quantify the statistics is the integrated luminosity.

Two methods for finding the position of the hot spot were studied, namely the standard deviation and the Gaussian fit method. Even though the y -distribution is non-Gaussian, the second method shows smaller uncertainties, both systematic and statistical. A possible explanation is that the standard deviation is more susceptible to the “noise”, such as the statistical fluctuations or background. The precision of the method obtained for the integrated luminosity of $200 \mu\text{b}^{-1}$ is already smaller than the pixel size ($50 \mu\text{m}$). With much larger statistics, expected of the LHC data, it should be possible to obtain even better precision.

We gratefully acknowledge prof. Janusz Chwastowski for many stimulating discussions and for his comments to the manuscript. This work was supported in part by the Polish National Science Centre grant UMO-2012/05/B/ST2/02480.

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