AUTOMATIC ANGULAR ALIGNMENT OF LHC COLLIMATORS

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Abstract

The Large Hadron Collider (LHC) is equipped with a complex collimation system to protect sensitive equipment from unavoidable beam losses. Collimators are positioned close to the beam using an alignment procedure. Until now they have always been aligned assuming no tilt between the collimator and the beam, however, tank misalignments or beam envelope angles at large-divergence locations could introduce a tilt limiting the collimation performance. This paper describes three different algorithms to automatically align a chosen collimator at various angles. The implementation was tested with and without beam at the SPS and the LHC. No human intervention was required and the three algorithms converged to the same optimal tilt angle.

INTRODUCTION

The CERN Large Hadron Collider (LHC) is the largest particle accelerator in the world, built to accelerate and collide two counter-rotating beams, each having a nominal energy of 7 TeV, with a design luminosity of $10^{34} cm^{-2} s^{-1}$ at a bunch collision rate of 40 MHz [1]. The LHC is susceptible to beam losses from normal and abnormal conditions [2,3] and must therefore be protected from any damage which may be caused by such beam losses [4].

The collimation system handles such beam losses and achieves a cleaning efficiency of 99.998% of all halo particles [4]. They are arranged in the form of a hierarchy with primary collimators (TCP) closer to the beam intercepting primary halo particles; secondary collimators (TCSG) retracted from the primary ones cleaning secondary particles; and tertiary collimators (TCT) with more retraction cleaning the remaining showers. In order to preserve this cleaning hierarchy the collimators need to be aligned with a precision of a few microns. The collimators are positioned in three planes; horizontal, vertical and skew, and are mainly concentrated in two dedicated cleaning insertions, IR3 (Insertion Region 3) and IR7 [4].

The current operational settings for the betatron cleaning hierarchy envisage a 1.5 σ retraction margin between the primary and the secondary collimators of the betatron cleaning insertion, which correspond to less than 300 μm. In order to push the performance of the LHC, tighter collimator settings with smaller retractions are foreseen, in order to achieve a lower β^* (related to the colliding beam size) and improved halo cleaning [5].

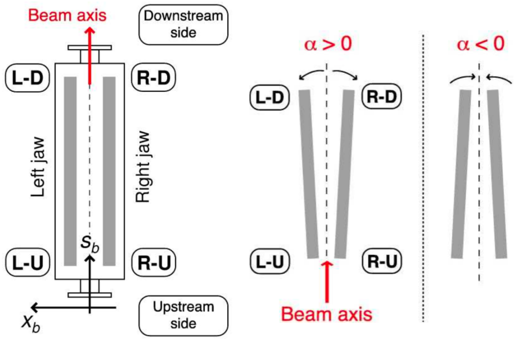
So far, collimators were aligned and operated with parallel jaws (zero tilt angle). Recent beam tests indicated that this approach will not be adequate to operate the system with retractions at 1.5 σ [6], therefore collimators need to be aligned at an appropriate tilt angle. At present, determining the best angle for a collimator would require one to manually apply an angular alignment method which is repeated for each LHC collimator. This motivated the development of an automatic software for efficiently performing angular alignments.

Over the years different elements have a tendency to move slowly due to ground motion. Having an angular alignment procedure that could be run at regular intervals (eg. on a yearly basis during the commissioning), would be useful to identify these issues early on. In addition, automating this would allow for exploring alignments at a larger angular range, and the different methods will be available for use on request. This was automated by aligning collimators using an established beam-based technique at different angles and the methods were tested without beam using a dedicated test-stand and then with beam in the Super Proton Synchrotron (SPS) and the LHC.

BACKGROUND

Collimator Coordinate System

In the LHC, ring-cleaning collimators are made of two jaws inside a vacuum tank and their coordinate system is displayed in Fig. 1a. Each jaw can be moved individually using dedicated stepping motors in the jaw corners with two degrees of freedom at either extremity, allowing collimators to be positioned at different angles, as displayed in Fig. 1b. The maximum and minimum possible angles are 1900 μrad and -1900 μrad respectively [8]. The jaw corners are known as left-up (LU) and right-up (RU) when they are upstream of the beam and left-down (LD) and right-down (RD) when they are downstream of the beam (or at the end of the beam).



(a) Jaw coordinate system (b) Jaw angular tilt convention

Figure 1: (a) The collimator coordinate system and (b) the jaw tilt angular convention as viewed from above, from [7].

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Standard Alignment Procedure

Beam-based collimator alignment is performed via a four-step procedure which was established in [9]. The procedure was tested with a prototype collimator in the SPS [10,11] and was first used in the 2010 LHC run [12]. The alignment of the collimators is beam-based as it can only be determined with beam in the machine. A collimator is considered aligned when a jaw movement towards the beam produces a clear loss spike in an assigned Beam Loss Monitor (BLM) detector located further downstream [4].

The standard alignment sequence involves aligning a reference collimator in addition to the collimator in question (collimator *i*) as is depicted in Fig. 2. The reference collimator is taken to be the primary collimator in the same plane (horizontal, vertical or skew) as collimator *i* which is to be aligned.

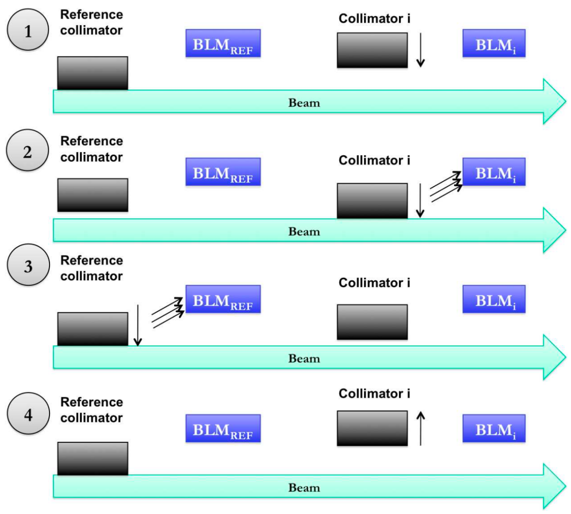

Figure 2: The four-stage beam-based alignment procedure for collimator i, using a primary collimator as a reference (only one jaw is shown for simplicity), from [13].

The first step is to move in the reference collimator jaws in steps towards the beam to form a reference cut in the beam halo. The second step is to align collimator *i* with respect to the reference halo generated earlier. Finally the reference collimator is realigned and collimator *i* is retracted to its position in the hierarchy [13]. The reference collimator is required to measure both the beam center and the beam size at collimator *i*.

Misaligned Collimators

The current alignment procedure has proved to be effective, however, until now, the collimators are aligned with zero tilt angle with respect to the beam. Figure 3 shows a jaw with an angular offset of α_i with respect to the beam axis, assuming that the two jaws are parallel in the collimator tank (ideal condition). Possible tank misalignments are a source of error that could jeopardise the performance of the system if not corrected.

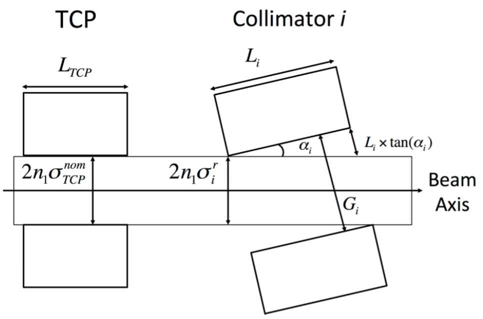

Figure 3: A case where collimator jaws are perfectly mounted with the vacuum tank, showing a tank misalignment w.r.t. the nominal orbit. Other cases involving mounting errors within the tank can also occur [13].

A change in the orbit or in the beam envelope along the collimator axis could also be compensated with the alignment of the collimator at an angle. The proposed solution is to implement an automatic procedure to align a collimator with different jaw tilts in order to be able to determine the best angle.

ANGULAR ALIGNMENT PROCEDURE

The principle of the angular alignment implementation is based on the standard alignment procedure discussed previously. Three different methods were implemented which align collimator *i* at different angles, one jaw at a time, such that ultimately the angle which produces the best results could be determined and used in operation.

Implementation

The software architecture designed for the collimation system is implemented in the LHC Software Architecture (LSA) [14]. The top-level consists of Java GUI applications that interact with the C/C++ Front-End Software Architecture (FESA) middleware, which implements real-time functionality, which in turn sends motor step commands to PXI-based systems. The collimators' left and right jaw positions and angles can be adjusted with a minimum step size of 5 μm, which is 1.82% of the 1 σ beam size at 7 TeV [4].

A new FESA class was implemented solely for the angular alignment and is responsible for aligning specific collimators as requested by the user. This class is executed for a selected collimator and requires a number of inputs:

- angle (α) - the largest angle in μrad, that defines the angular range explored in the procedure
- angle step size (δ) - the step size in μrad, at which collimator *i* will be tilted between each alignment
- operation - a flag that identifies which of the three methods to execute
- BLM threshold for collimator *i* - this defines the BLM threshold to be used when aligning collimator *i*

- BLM threshold for primary collimator - this defines the BLM threshold to be used when aligning the primary collimator as a reference for collimator *i*

METHOD 1: Angular Alignment using Reference Collimator

This method is heavily based on the standard alignment procedure. The main difference is that collimator *i* is tilted at a pre-defined angle before alignment. To run this method, the user selects a collimator *i*, then sets α and δ (e.g., 1000 μrad and 100 μrad respectively), and the following procedure is performed automatically:

1. Align the corresponding reference collimator and collimator *i* as shown in Fig. 2 (angle: 0 μrad)
2. Tilt collimator *i* to α (angle: 1000 μrad)
3. Align collimator *i* at the angle set, then re-align the reference collimator (angle: 1000 μrad)
4. Tilt collimator *i* by δ (angle: 900 μrad)
5. Repeat steps 3 and 4 until the angle -α is reached (final angle: -1000 μrad)
6. Tilt collimator *i* back to its initial angle (angle: 0 μrad)
7. Retract the reference collimator to its starting position

This method produces the positions of both collimators after each alignment, at angles between the largest angle and its negation. As a result the best angle can be extracted by identifying the angle which generates the smallest measured beam sigma.

METHOD 2: Angular Alignment at Maximum Angles

This method does not require a reference collimator or any user inputs. The method applies the following steps on the selected collimator *i* automatically:

1. Retract collimator *i* by 2 mm
2. Tilt at maximum angle (1900 μrad) to find the upstream center as shown on the left in Fig. 4.
3. Align collimator *i* then retract by 2 mm
4. Tilt at opposite maximum angle (-1900 μrad) to find the downstream center as shown on the right in Fig. 4.
5. Retract collimator *i* by 2 mm

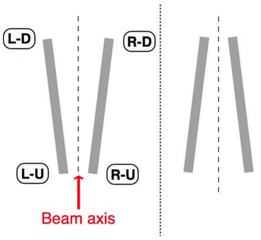

Figure 4: Jaws open at maximum angles

This method produces the upstream and downstream centers of the collimator and these can be used to calculate the optimum angle. This is the quickest method out of the three as it simply requires two alignments to be performed.

METHOD 3: Angular Alignment using a Jaw as Reference

This method does not require a reference collimator, as it treats the two jaws of collimator *i* separately, such that one jaw acts as the reference and the other jaw is tilted at different angles. Running this method requires the same parameters as the first method, whereby the user selects a collimator i, then sets α and δ (e.g., 1000 μrad and 100 μrad respectively), and the following procedure is performed automatically:

1. Align the collimator *i* (collimator *i* angle: 0 μrad)
2. Retract the left jaw of collimator *i* and tilt it to α (left jaw angle: 1000 μrad) as show on the left of Fig. 5
3. Align the left jaw at the angle set (left jaw angle: 1000 μrad)
4. Align the right jaw as a reference (right jaw angle: 0 μrad)
5. Retract the left jaw and tilt it by δ (left jaw angle: 900 μrad)
6. Repeat the above three steps until the angle -α is reached (left jaw final angle: -1000 μrad)
7. Tilt the left jaw back to its initial angle (collimator *i* angle: 0 μrad)
8. Retract collimator *i* by 1.2 mm
9. Repeat all steps 1-8, this time by tilting the right jaw and keeping the left jaw as a reference as shown on the right in Fig. 5.

This method produces the positions of both jaws after each alignment, at angles between the largest angle and its negation, for both the left and right jaws separately. As a result the best angles for the left and right jaws can be extracted. This method takes approximately the same amount of time as the first method.

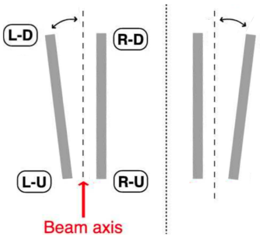

Figure 5: Single jaw at an angle with other jaw as reference

Calculations

For each alignment at an angle, the measured beam σ can be calculated, and the angle which results in the minimum value is the most optimal one. This is due to the fact that the angle resulting in the lowest measured beam σ implies that the collimator is the most parallel to the beam axis at the given angle, recall Fig. 1.

The different methods produce different data, therefore the way the measured beam σ is calculated varies according to the method used.

- **Method 1**: This method is based on the fact that if there is a misalignment of collimator *i* with respect to the beam, the measured beam size of the collimator will be larger than the real one. This method gives the positions of the aligned angular collimator at each angle, as well as the position of the aligned reference collimator before and after aligning the angular collimator. These positions are used in Eqn. 1 to calculate the jaw gap.

$$G_i = x_i^{L,m} - x_i^{R,m}, \tag{1}$$

where $x_i^{L,m}$ and $x_i^{R,m}$ are the measured left and right jaw setup positions. The half gap is then used to calculate the measured beam size using:

$$\sigma_i^{meas} = \frac{G}{(N\sigma_{ref_1} + M\sigma_{ref_2})/2}, \tag{2}$$

where $N\sigma_{ref_1}$ is the Nσ of the reference collimator before aligning the angular collimator and $M\sigma_{ref_2}$ is the Mσ of the reference collimator after aligning the angular collimator. In both cases, σ_{ref} is calculated from the nominal geometrical emittance and nominal β.

- **Method 2**: This method gives the left and right positions after aligning the upstream and downstream jaw corners separately. From these positions the upstream and downstream centres can be calculated using Eqn. 3 and then the angle can be calculated using Eqn. 4.

$$\Delta x_i^{up} = \frac{x_i^{LU,m} + x_i^{RU,m}}{2}, \ \Delta x_i^{down} = \frac{x_i^{LD,m} + x_i^{RD,m}}{2} \tag{3}$$

$$\theta = \Delta x_i^{down} - \Delta x_i^{up} \tag{4}$$

- **Method 3**: This method is based on the same concept of monitoring the collimator *i* measured beam size as a function of the angle, this time using one jaw as a reference. This method gives the position of the aligned angular jaw at each angle and the position of the aligned reference jaw before and after aligning the angular jaw. Eqn. 5 is then used to calculate the measured σ at each of the angles aligned.

$$\sigma_i^{meas} = \frac{\Delta x_i - \Delta x}{(N\sigma_{jaw_1} + M\sigma_{jaw_2})/2}, \tag{5}$$

where Δx_i is the average of the up and down positions of the aligned jaw at an angle, in millimetres, Δx is the center of the collimator jaws when aligned with zero angle, in millimetres, $N\sigma_{jaw_1}$ is the Nσ of the reference jaw before aligning the angular jaw and $M\sigma_{jaw_2}$ is the Mσ of the reference jaw after aligning the angular jaw.

RESULTS FROM BEAM TESTS

The LHC contains 21 collimators which have beam position monitor (BPM) pick-up buttons embedded in the collimator jaws. BPMs are able to directly provide a measurement of the beam orbit at the collimators and therefore are able to align collimators more quickly when compared to the standard technique which relies on feedback from beam losses [15].

SPS Results

The methods were first executed in the SPS, using coast beam at 270 GeV, with one LHC type nominal bunch having an intensity of 1.1E11p. The BPM prototype collimator in the SPS, TCSM.51934, was aligned using each method and the results displayed in Fig. 6 were obtained. All results are normalized by using:

$$\sigma_i^{norm} = \frac{\sigma_i^{meas} - min(\sigma_i^{meas})}{max(\sigma_i^{meas}) - min(\sigma_i^{meas})} \tag{6}$$

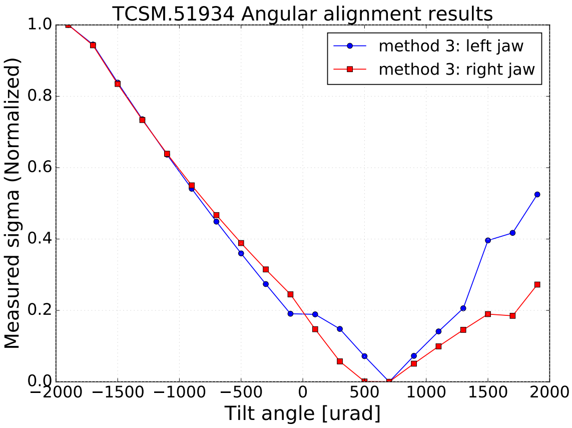

Figure 6: The normalized measured beam σ for different tilt angles for the SPS beam test with the TCSM.51934 collimator (BPM align: 700 μrad, method 2: 550 μrad)

Since the SPS has only one LHC-type collimator where the position of both jaws is known with respect to a common zero position (i.e. the centre of the beam pipe), the method which requires a reference collimator had to be done using a scraper instead. The scraper is another device for scraping beam and has a different reference system. Its jaw position is the absolute one starting from zero at parking and therefore it is not possible to calculate the gap between the two jaws, which is required to calculate the Nσ as required in Eqn. 2. The results using methods 2 and 3 indicate that the most optimal angle is approximately 600 μrad.

LHC Results

The methods were then executed in the LHC at injection (450 GeV) using one nominal bunch at an intensity of 1.1E11p. The BPM collimators were all aligned with their respective BPMs in order to quickly determine the collimator with the largest tilt angle in beam 2. The TCTPH.4R2.B2 which is a tertiary horizontal collimator in IP2 beam 2, was found to have the largest tilt, therefore this was aligned using the three angular alignment methods, and the results are shown in Fig. 7. The time taken for each of the three methods are: 22 minutes for method 1, 5 minutes for method 2 and 15 minutes for method 3.

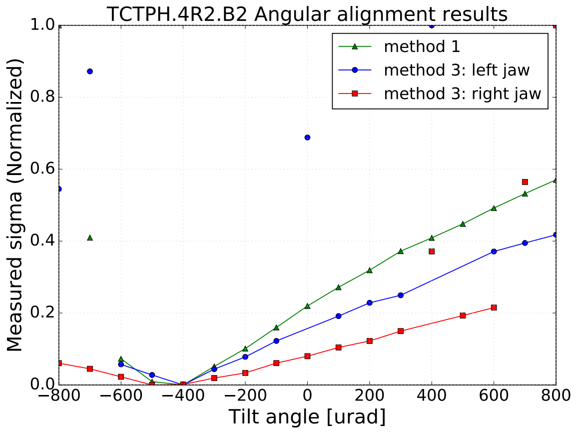

Figure 7: The normalized measured beam σ for different tilt angles for the LHC beam test with the TCTPH.4R2.B2 collimator (BPM align: -490 μrad, method 2: -410 μrad)

The plot in Fig. 7 shows a number outliers which are the results obtained when the jaw was stopped earlier at fake loss spikes, since a semi-automatic alignment algorithm was used. This is seen by the automatic software as it indicates an aligned position while the jaw is still apart from the reference halo. A more robust and fully automatic alignment algorithm based on spike recognition is planned to improve it.

The results using each of the methods indicate that the most optimal angle is approximately -450 μrad. In addition, a separate test was performed whereby this collimator was first aligned with zero angle using the BLMs. The collimator was then retracted and aligned with BPMs in order to obtain the optimal angle parallel to the beam axis. The collimator was then re-aligned at this angle using the BLMs. The beam size ratio obtained with aligning an angle was 24% less than that obtained when aligning without an angle. This highlights the significance of identifying the optimal angle for a collimator before alignment.

CONCLUSION

This paper describes the implementation and beam tests of three angular alignment methods to determine optimum angular settings for the LHC collimators. The implementation was successfully tested with beam, achieving an automatic angular alignment at 450 GeV and 6.5 TeV, with no human intervention. The results obtained from aligning a collimator using the three methods indicate that the most optimal angle can indeed be obtained using any of the methods.

Selecting which method to use depends on the specific error encountered and can therefore only be determined with more operational experience with angular setups. Methods 1 and 3 are similar as they both align the collimator at various angles, the main difference being that method 1 keeps the jaws parallel to each other. Method 1 would be ideal for cases where there is a real offset of the tank, as the requirement that the collimator jaws are parallel would be met. On the other hand, method 3 would be useful in cases of asymmetries within the collimator itself, as this method is able to determine the most optimal angle for each jaw independently. Method 2 is the fastest method which is able to quickly calculate the upstream and downstream centres.

Overall, all methods were able to converge to the same angle for the collimator tested in the first measurements. Future work involves enhancing the alignment algorithm in order to automatically determine whether a collimator is aligned with the beam or not using spike recognition, as this would transform the semi-automatic alignment to a fully-automatic one.

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