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Alignment strategy for the LHCb vertex locator

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LHCb is one of the four main experiments of the Large Hadron Collider (LHC) project, which will start at CERN in 2008. The experiment is primarily dedicated to B-Physics and hence requires precise vertex reconstruction. These requirements place strict constraints on the LHCb vertex locator (VELO) alignment. Additional challenges arise from the VELO being retracted between each fill of the LHC and from its unique circular disc R/Φ strip geometry. This paper describes the software alignment procedure developed for the VELO, which is primarily based on a non-iterative method using a matrix inversion technique. The procedure is demonstrated with simulated events, and results obtained during runs in external test-beams are also presented.

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1. Introduction

LHCb is the dedicated heavy flavor physics experiment at the LHC. The physics goals are critically dependent on the performance of the precision vertex locator (VELO). Whilst the intrinsic VELO sensor single hit resolution is $5-10$ μm for all tracks in the acceptance, the sensors also have to be retracted by 3 cm from the unstable LHC beams while the machine is filled. As a result of these very unique constraints, described in Section 2, the VELO has particularly complex alignment requirements.

The VELO has been assembled with a high precision and a detailed metrology has been performed. However, the only possible method for correcting misalignments during data taking is through a track-based software alignment procedure. A new alignment will be performed after each re-insertion of the VELO, in order to ensure optimal data taking. The 'three steps' procedure is described in Section 3. Then, results obtained using simulated events are described in Section 4. The performance of the first two phases of the alignment process were also tested on data collected during VELO beam tests. The results of this study are presented in Section 5. Finally, summary and conclusions are given in Section 6.

2. The VELO Alignment Context

The VELO consists of two retractable halves, each with 21 modules. Each module contains two semi-circular silicon strip sensors that measure R (radial) and Φ (azimuthal angle) co-ordinates, respectively. Further details on the VELO design can be found elsewhere in these proceedings [1, 2, 3].

The successful operation of the LHCb trigger puts demanding constraints on the VELO assembly precision, as it heavily relies on a very precise vertexing. Moreover, uncorrected misalignments could have significant effects on the trigger performance. For example, a rotation of 0.5 mrad around the Y-axis of one detector can reduce the trigger efficiency by 30% for the $B_s \to K^+K^-$ channel [4].

3. The VELO Alignment Procedure

The alignment of the LHCb VELO proceeds in a number of stages: precision assembly; metrology; and software alignment.

A survey of the VELO system has been performed. The relative position of the R and Φ sensors on a single module have been measured to an accuracy better than 5 μm, and no significant curvature of the sensors was observed. The relative position of the VELO modules on the VELO half bases has also been determined with a similar precision. The survey is of particular importance for determining degrees of freedom that can be constrained less well from tracks, such as the relative z-positions of the VELO modules.

Then, the VELO software alignment procedure is divided into three phases:

- The relative alignment of R and Φ sensors within one VELO module [5].
- An internal alignment of the modules within each VELO detector-half [6].

- A relative alignment of the two halves with respect to each other [7].

The first part of the procedure was not fully operational at the time of the conference, hence only the two last phases are described in the following sections.

3.1 Relative Module Alignment

The second step of the alignment procedure is to perform the relative alignment of the 21 VELO modules within one detector-half. This is based on a non-iterative χ^2 minimization method using a matrix inversion technique.

The χ^2 is produced from the residuals between the tracks and the measured clusters. The measured residuals are expressed as a linear combination of the track parameters and the alignment constants. Each straight line track has four parameters (two slopes and two intercepts) denoted by n_{local}. The total number of translational and rotational degrees of freedom of all the modules is n_{global} alignment constants. The track fitting and alignment problem can then be expressed as a system of n_{total} equations, where n_{total} is given by

$$n_{total} = n_{local} \cdot n_{tracks} + n_{global}.$$

Clearly, the size of the system scales with the number of tracks used in the alignment. As we will see later, about 20,000 tracks are necessary to obtain a detector-half alignment of the required accuracy. Hence, this implies solving a system of over 80,000 equations, which is a computationally challenging task. However, this problem can be reduced to the size of n_{global} (around 100 for the VELO) using the technique of matrix inversion by partition, performed by the program Millepede[1] [8] .

An important component of the alignment procedure is the selection of the track sample used. In order to ensure an optimal population of the final matrix, a mixture of tracks coming from the primary interaction point and a complementary set of tracks from the beam halo or beam-gas interactions will be used. A specific pattern recognition algorithm has been developed in order to select these events [9].

The ‘weak-modes,’ *i.e.* deformations which are difficult — if not impossible — to unfold with tracks, are extensively constrained, via constraint equations (to prevent global linear deformation of the system) and χ^2 ‘penalty-terms’ (to constrain weak degrees of freedom).

The results of applying this second step of the alignment procedure to simulation events are given in section 4.1.

3.2 Detector-halves Alignment

The final step of the alignment procedure is to perform the relative alignment of the two detector-halves. Clearly, the module residuals within a detector-half are not sensitive to the mis-alignment of the whole half. Thus, observables connecting the two detector-halves are needed here.

Overlap tracks, i.e. tracks that pass through both VELO detector-halves, provide a powerful constraint for the relative positioning of the two detector-halves. These tracks are required to have

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[1] a `C++` translation of the `FORTRAN` Millepede program has been implemented by the authors of Ref. [6].

at least one (r,ϕ) cluster pair (spacepoint) in each VELO detector-half. The VELO was specifically designed to obtain such a class of tracks. The overlapping area between the two VELO detector-halves, when fully inserted, corresponds to 2% of the active surface area of the sensors.

Having selected these special tracks, the alignment proceeds by residual minimization using the same technique as the module alignment. The matrix inversion technique allows to determine the six relative alignment constants of the detector halves, assuming the VELO is fully inserted for physics data taking.

However, during insertion and during the commissioning phase an alignment may be required with the VELO in the retracted position. In this case the rate of overlap tracks becomes very small and an alternative technique is required. The detector-half alignment can then be performed using vertices as constraints. Tracks from the primary interaction point can be used if available or beam-gas interactions occurring in the VELO vacuum tank. By fitting for the vertex[2] separately inside each of the two detector-halves, one can obtain the misalignment between the two halves.

More details on this novel technique of alignment with vertices can be found in Ref. [7]. The vertex fitting method can also be used to determine the VELO 'detector-halves' positions with respect to the beam, when using vertices from the primary interaction point.

The results of applying this final step of the alignment procedure to simulation events are given in section 4.2.

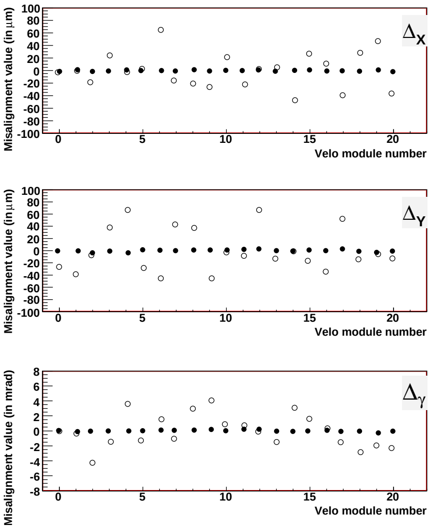

Figure 1: Misalignment values before (○), and after (●) internal alignment, for one particular configuration.

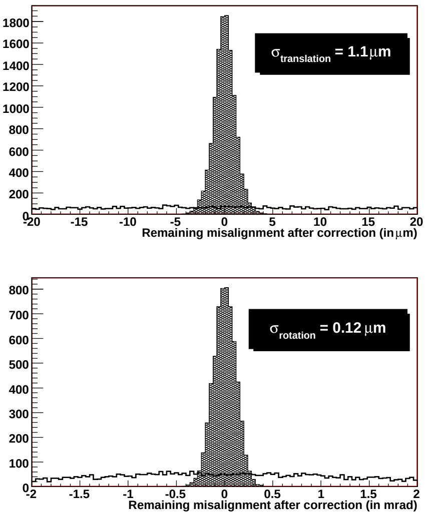

Figure 2: Misalignment values before (□), and after (■) detector halves alignment, for all configurations.

4. Simulation Studies

A simulation of 200 samples of 25,000 events each has been produced and propagated through the LHCb software. Each sample, which comprises a mixture of 5,000 minimum bias events

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[2] The Millepede framework is still applicable as it does not depend on the object that is being fitted.

(≈ 100,000 tracks from primary vertex interactions) plus 20,000 beam-halo like events, was produced with a different set of alignment constants. The misalignment values have been randomly chosen within a Gaussian distribution centered on zero and with resolutions based on construction and survey accuracies (defined in Ref. [7]). All the module and detector-half degrees of freedom have been misaligned.

4.1 Relative Module Alignment Results

The internal alignment of the modules in each detector-half is particularly sensitive to translations of the modules in the X and Y directions ($\Delta_{X,Y}$) and rotations around the Z-axis (Δ_{gamma}). Results on the alignment of all modules in a detector-half, for one particular sample, are presented on Fig.. 1. On Fig. 2 the alignment constants for 200 event samples, before and after correction, are shown. Resolutions of the X and Y translation alignment parameters of 1.1 μm and on rotations around the *z*-axis of 0.12 mrad are obtained. About 20,000 tracks per detector-half were needed to obtain this accuracy. The alignment resolutions are well below the intrinsic detector hit resolution.

4.2 Detector-halves Alignment Results

Although the three alignment steps can be performed separately, in practice it is expected that steps two and three will be run consecutively. Hence, the results presented in this section are for the realistic case of performing both of these alignment steps on misaligned samples. The tracks are refitted after the module alignment procedure in order to update the track parameters. The results presented here have been obtained with about 300 overlap tracks.

The results of the study are presented on Fig. 3. The resolution on the X and Y translation alignment parameters is 12 μm for x and y translations, and the resolution on the x and y tilts is 36 μrad.

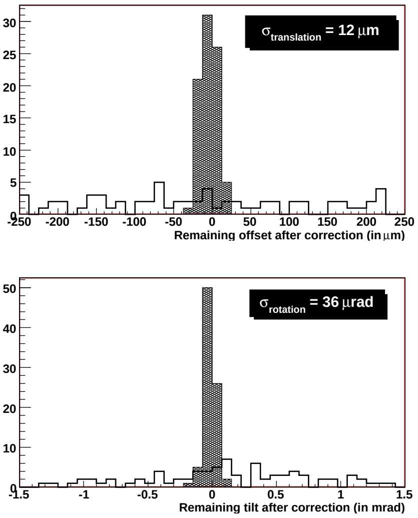

Figure 3: Misalignment values before (□), and after (■) detector halves alignment, for all configurations.

5. Results on testbeam data

Several alignment challenge and detector commissioning (ACDC) phases were carried out in 2006 by the LHCb VELO group in order to facilitate the installation of the detector. ACDC3 phase was carried out with a partially equipped VELO detector half that was placed in an external test beam. Ten out of the 21 modules were installed in their final setup. There was enough electronics available to read-out six out of the ten modules simultaneously, and the detector half was operated under vacuum (10^{-3} mbar) with modules cooled down ($< 0\ ^{o}$C).

5.1 Principle

One of the main purpose of the ACDC3 campaign was to test the alignment procedure in conditions close to the final setup. Moreover, as the VELO is a moving detector, it was also an unique occasion to evaluate the system sensitivity to hardware operation like translation or pumping.

The alignment constants were determined using the software procedure described previously. Alignment files were produced for each cabling configuration[3], using the most complete set of tracks available in order to get the best possible result (i.e. the most uncorrelated one). Results presented here were obtained with configurations 1 and 4, using mainly the target runs, as they contained both perpendicular and angled tracks.

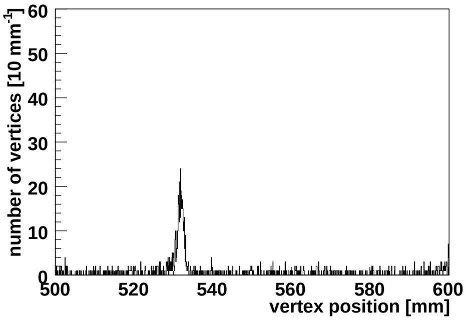

Figure 4: Vertices reconstructed in target 3 & 4 before the alignment procedure.

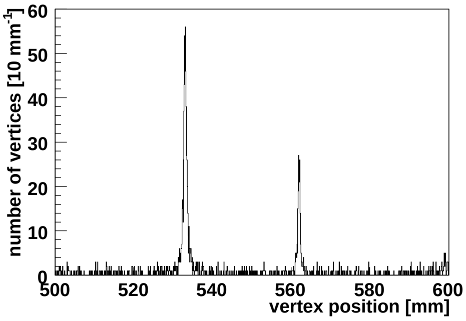

Figure 5: Vertices reconstructed in target 3 & 4 after the alignment.

5.2 Effect on vertexing

LHCb trigger is based on a precise separation of B decays vertices from the primary vertices. To this end, a very good vertexing accuracy is crucial for the experiment.

This effect is illustrated on Figs. 4 and 5. These plots were obtained by running the alignment on the same set of target events, using the same tuning for the pattern recognition. On Fig. 4 no alignment correction is applied, and it is clear if we look at the reconstructed vertices, that only one target is visible. Figure. 5 shows what happens when the full alignment information is included: the second target appears, and one gets much more reconstructed vertices.

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[3] In total, four different cabling configurations were tested.

5.3 Effect on resolution

The VELO sensor resolution has been studied mainly using tracks of perpendicular incidence. The resolution has been determined as the sigma of a gaussian fit to the distribution of unbiased residuals for a given region in pitch. The small angle of the tracks (less than 2 mrad) means that their hits all lie in the same pitch region with negligible effects at the border of two pitch regions.

To obtain the resolution one has to correct for the extrapolation error of the track fit which contributes to the measurement. Under the assumption that all sensors have equal performance and that all track hits are in the same pitch region, i.e. all hits should have the same hit resolution, one can compute the relative contribution of the extrapolation error to the residuals [10]. The thus obtained correction factors can be applied to the fitted resolutions.

Figure 6 shows the VELO sensor resolution averaged over 6 R and Φ sensors. Higher values for very small and very large pitch regions are due to very limited statistics.

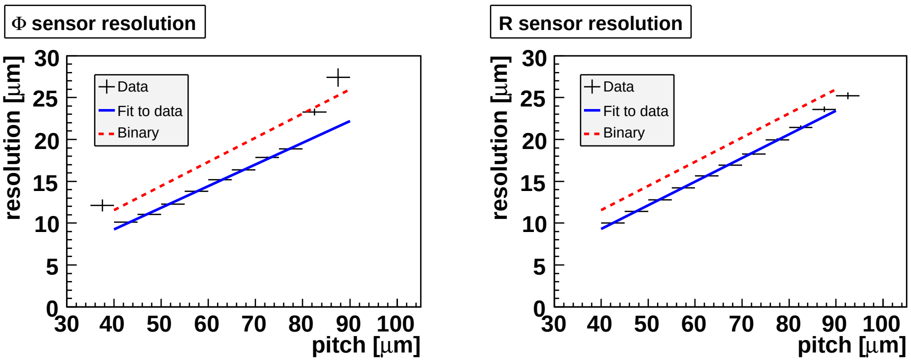

Figure 6: Φ (left) and R (right) sensor resolutions, averaged over 6 sensors.

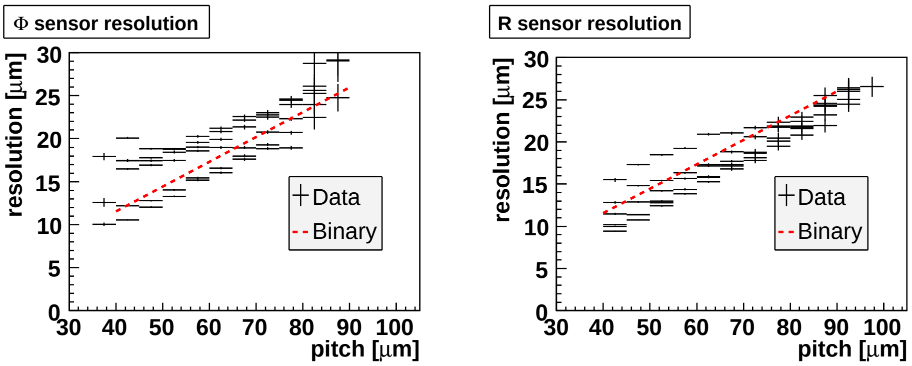

Figure 7: Φ (left) and R (right) sensor resolutions for the 6 read-out sensors.

The resolution performance without using any misalignment or metrology information is shown on Fig. 7. As can be seen the resolution is deteriorated significantly. However, it is much worse for ϕ sensors than for R sensors. This can be understood as the assembly process was such that the R sensor was placed with a higher precision, which is motivated by the R-Z-tracking in the trigger being based on R sensor information only.

6. Conclusion

A software alignment method for the LHCb vertex locator has been developed. This procedure performs the alignment in three steps, all based on track residuals. First, a relative alignment of the R and Φ sensors within each VELO module is performed. This is followed by an internal alignment of the VELO modules within each detector-half. Finally, since the detector-halves are moved between each LHC fill, a final step is required in order to align the detector-halves with respect to each other, thus providing a fully internally aligned VELO.

The final two stages[4] of VELO alignment strategy use the Millepede program, which enables the alignment to be performed in only one pass; this is to be compared with classic minimization methods which require many iterations to provide their result. This technique allows the processing of module and VELO-half alignment within a few minutes on a single CPU[5], assuming that an appropriate data sample has been collected. Future work will be undertaken to enable an efficient selection of the required tracks in the LHCb trigger.

For the internal alignment of the modules in a detector-half a 1.1 μm precision has been achieved on the major translational degrees of freedom (*i.e.* along X and Y axes), and a 0.1 mrad accuracy on the rotation around the Z-axis. These precisions are well below the expected detector intrinsic resolution.

The results of the detector-half alignment procedure show that the tracks that pass through the overlap region between the two VELO detector-halves provide a very strong constraint. With only a few hundred tracks accuracies of 12 μm for x and y translations, and 36 μrad for X and Y tilts, are obtained. These results are also well within the system requirements.

The procedure was also tested during November 2006 testbeam runs. The alignment information obtained has largely improved tracking and vertexing performance. Also a significant improvement of the detector resolution, due to the alignment information, was observed, thus proving the efficiency of the software alignment procedure on real data.

References

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[4] The first stage was not described here as it was not completely ready at the time of the conference.

[5] 1 CPU = 1000 SpecInt2000 units