1. Overview of the trigger and real-time analysis

- The data volume generated from the LHCb detector currently reaches 5TB/s [1].
- To record the data to permanent storage, this rate is reduced by a factor 400 by the trigger system [2], which uses fully reconstructed events to select specific signals of interest.
- This approach is called real-time analysis [3]: requires an offline-quality reconstruction enabled by the alignment and calibration of the detector performed in quasi-real-time (Figure 1):
  - **HLT1**: Run in GPUs. Performs a partial reconstruction and reduces data volume by a factor 20 [4].
  - **Alignment and Calibration**: Ensures the physics parameters are computed with the best possible resolution.
  - **HLT2**: Run in CPUs. Performs a full offline-quality reconstruction and selection of physics signatures.

![Figure 1: Online dataflow](image)

2. Aspects of HLT2

2.1. Reconstruction

The offline-quality reconstruction is divided into four main components:

- **Charged particle pattern recognition**: Tracking algorithms that use information from VELO, IT and SciFi detectors according to different track types (Figure 2).

![Figure 2: Example of track seeding and extension in the VELO pattern recognition algorithm](image)

- **Calorimeter reconstruction**: Build clusters from ECAL detector (Section 3) and match them with the extrapolation of reconstructed tracks.

- **Kalman filter**: Achieve best accuracy and precision of tracks with a Kalman filter based algorithm (Figure 3).

![Figure 3: Relative momentum resolution of reconstructed tracks as a function of momentum](image)

- **Particle Identification**: Information from the two RICH detectors [6], ECAL and the muon system [7] is used to identity charged particles. Optimal performance is achieved with machine learning algorithms.

![Figure 4: Spectrum of the p T COSH, normalized to the degrees of freedom, for muons and pretensor samples. Evaluated with Run 2 data](image)

2.2. Selection

- The selection process relies on O(1000) selection algorithms tuned for a particular signal topology or physics analysis that can use multivariate or artificial intelligence models. An example of selected candidates is shown in Figure 5.
- After the selection algorithms, the information is sent to three streams according to its purpose: full stream, Turbo stream and TurbC stream [8].

![Figure 5: Mass difference of selected P(2010) candidates](image)

3. Example of an improved reconstruction algorithm: Calo Graph Clustering

- **Graph Clustering** is the new default solution for ECAL reconstruction, maintaining the efficiency of the previous algorithm and improving by 65.4% the execution time on average (Figure 6).
- It uses graph data structures to store event data.
- Using a set of rules, it inserts the digits into the graph to create cluster structures (Figure 7).
- It analyses the connected components solving the overlapping cells between clusters in a dedicated algorithm.

![Figure 6: Complexity comparison between Cellular Automata and Graph Clustering](image)

![Figure 7: Examples of graph structures](image)

4. Alignment and Calibration

- Provides the most accurate alignment and calibration parameters for reconstruction and selection.
- Each step is performed with a different frequency [13, 14]:
  - Full tracking system: aligned at the beginning of each fill within few minutes.
  - Calorimeter calibration: evaluated every 2 weeks.
  - RICH calibration: evaluated on run basis. Mirror alignment performed for each fill within few tens of minutes.
  - Muon alignment: run as monitoring.

- **First alignment of the tracking system on Run 3 data has been evaluated** (Figure 9, 10).

![Figure 9: Misalignment of the VELO halves evaluated as the difference in a position of the PVs on each VELO half, for different alignment conditions](image)

![Figure 10: Tracking performance for different alignment conditions using VELO and SOFT](image)

- **ECAL calibration** requires to adjust the gain of PMTs using a LED reference value after each fill [15].
- A more fine-grained calibration is based on the observed 37 mass on each cell (Figure 11).

![Figure 11: m# photon invariant mass after per-cell calibration](image)

References: