Time-dependent amplitude analysis of $B^0 \to K^+K^-K_S$ at the LHCb experiment

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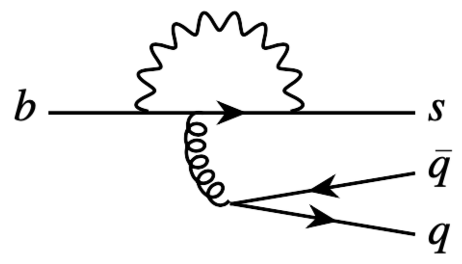
The $B^0 \to K^+K^-K_S$ charmless three-body decay

The dominant contributions to the Feynman diagram of $B^0 \to K^+K^-K_S$ come from $b \to sq\bar{q}$ penguin diagrams (where q is a u, d or and s quark).

Branching franctions are of order of 10^{-5}.

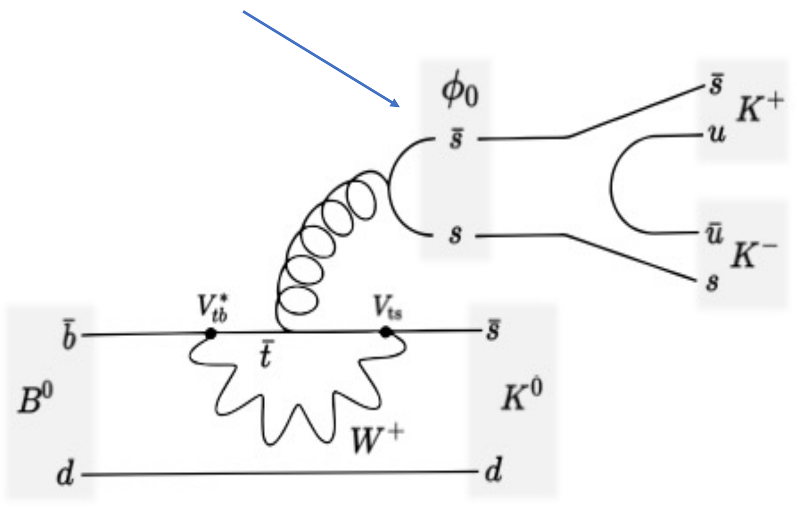
Virtual particles circulating in the loops can introduce experimental deviation from the Standard Model.

Compare SM predictions to precision measurements.

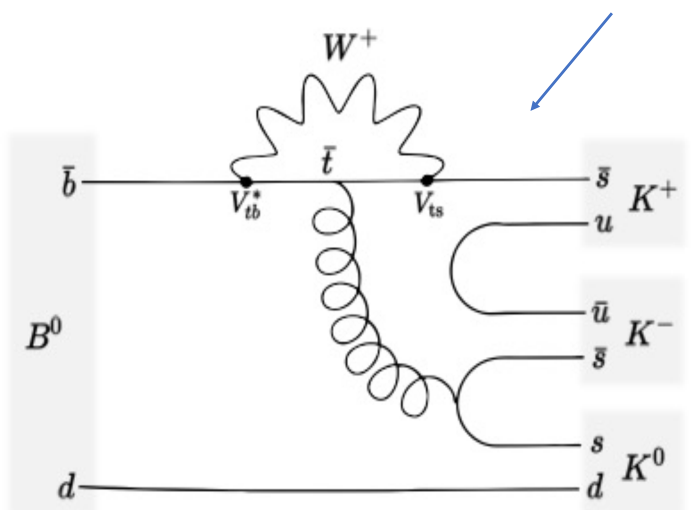


Building block of charmless three-body B^0 decays.

Charmless resonance



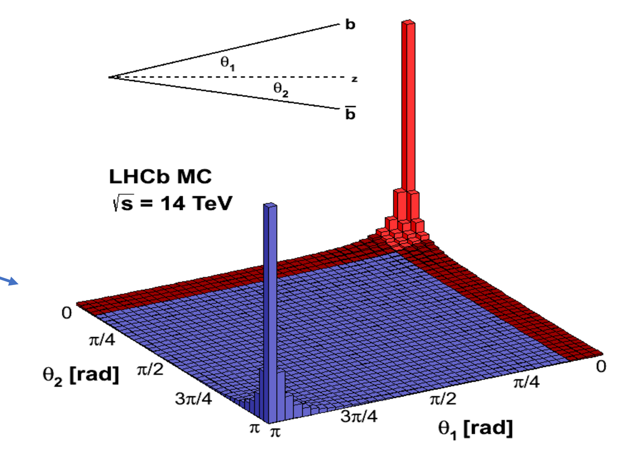
Non-resonant process



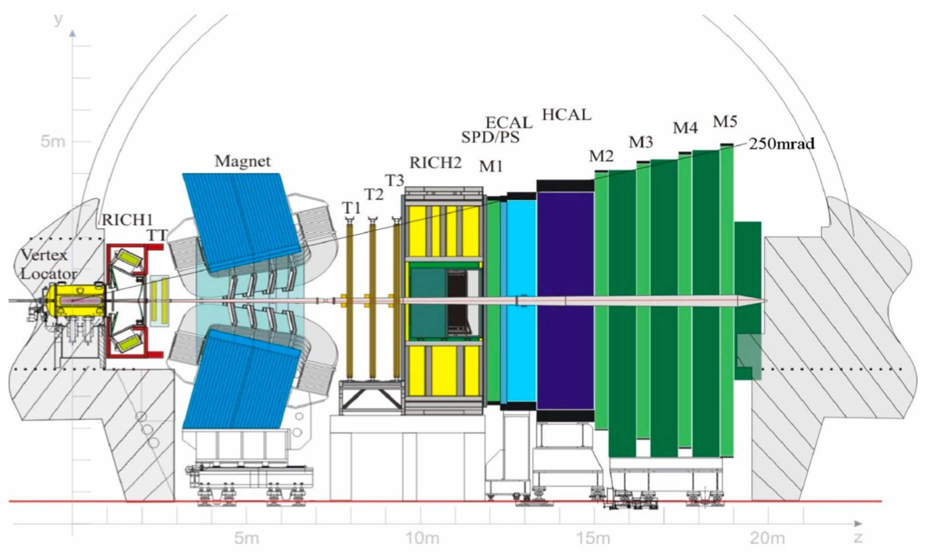
The LHCb detector at CERN

LHCb is a single-arm forward spectrometer, designed for the study of particles containing b or c quarks.

LHCb narrow-angle structure ($2 < \eta < 5$) is thought to exploit the fact that $b\bar{b}$ pairs in pp collisions are produced in the forward region.

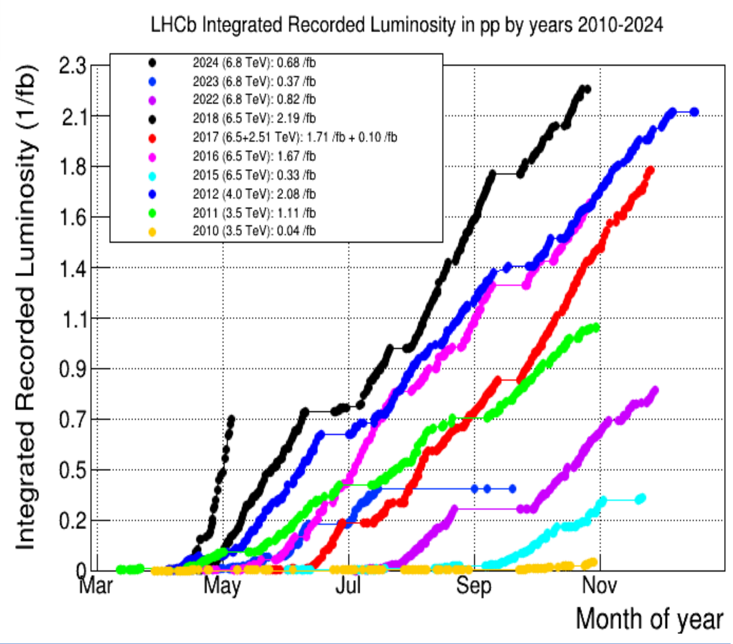


Good PID discrimination and resolution of secondary vertices.



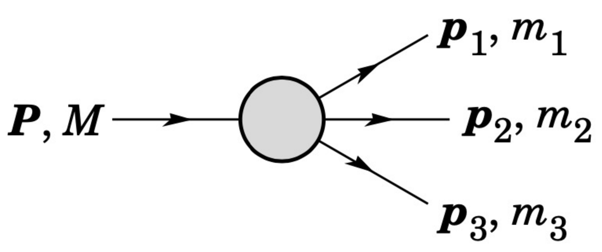
LHCb detector design and components at Run2 time.

In LHC-Run3 10 + 10 fb^{-1} more data will be recorded, more than doubling the luminosity in Run1+2 of 9 fb^{-1}.



Amplitude analysis of a three-body decay

In a three-body decay, 2 d.o.f (i.e. m_{12}^2, m_{23}^2) are needed to describe the phase space → Dalitz plot.



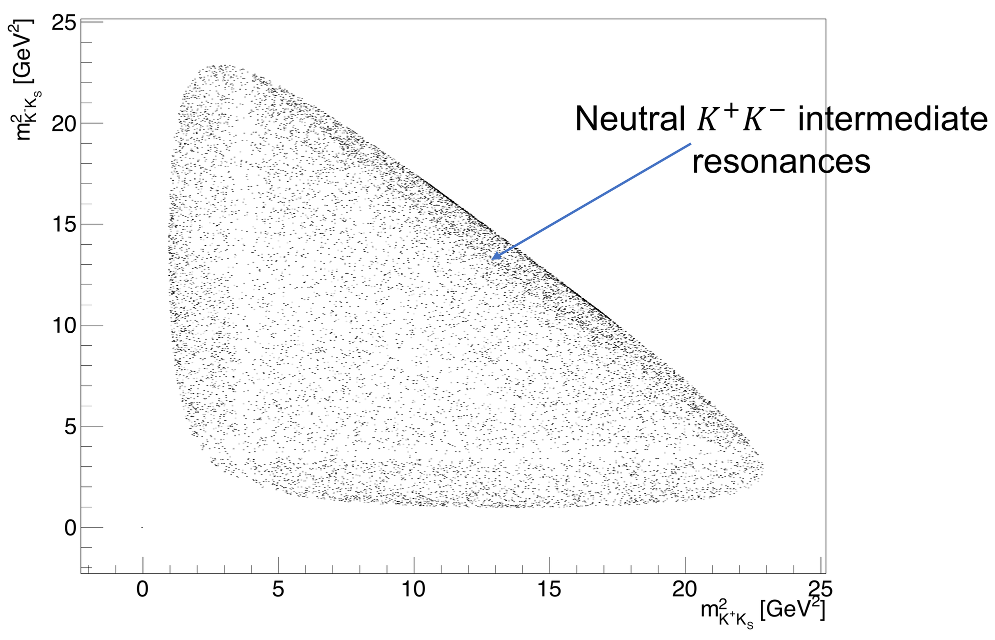
Intermediate resonances
(i.e $B^0 \to \phi(\to K^+K^-)K_S$) cause non-uniformity of the amplitude A over the Dalitz plot.

Amplitude analysis: fit an amplitude model to the Dalitz-plot distribution to extract physics observables.

In the Isobar model, the total amplitude is given by the sum of intermediate-state amplitudes:

$$A(m_{12}^2, m_{23}^2) = \sum_{j=1}^{N} A_j(m_{12}^2, m_{23}^2)$$

The quantum interference between resonances gives access to relative phases.



Dalitz plot of $B^0 \to K^+K^-K_S$ data. 2018, DD, LHCb unofficial.

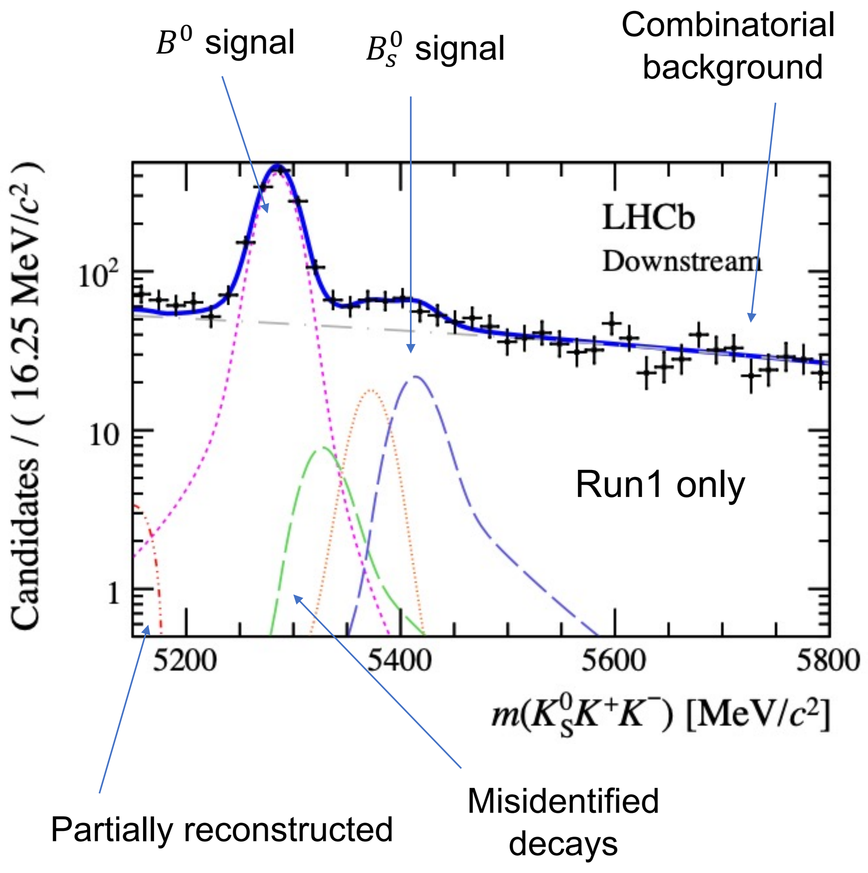
Analysis strategy and goals

LHCb has only investigated the global branching ratio of $B^0 \to K^+K^-K_S$.

With the increase of luminosity in Run3, a time-dependent Dalitz-plot analysis will become feasible.

The signal Dalitz-plot distribution to use in the amplitude analysis is extracted from the invariant-mass fit (sPlot).

Measure of the **CP violation in each of the intermediate modes**.



[1] *LHCb collab.* "Updated branching fraction measurements of $B^0_{(s)} \to K^+K^-K_S$ decays". arXiv: 1707.01665 [hep-ex]

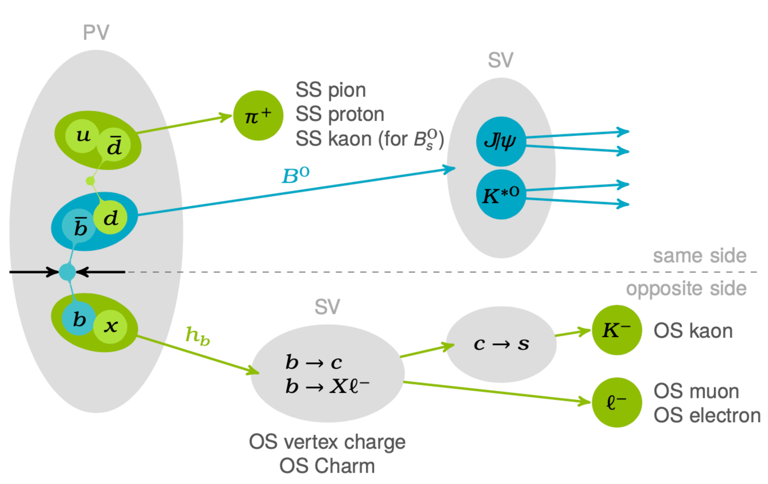
[1] Fit to the $K^+K^-K_S$ invariant-mass spectrum in the LHCb Run1 branching-fraction analysis.

Flavour tagging at LHCb

Time-dependence in the amplitude analysis implies taking into consideration the oscillation of the $B^0/\overline{B}^0$ system.

Tag the flavour of the B^0 / $\overline{B}^0$ at the time of production.

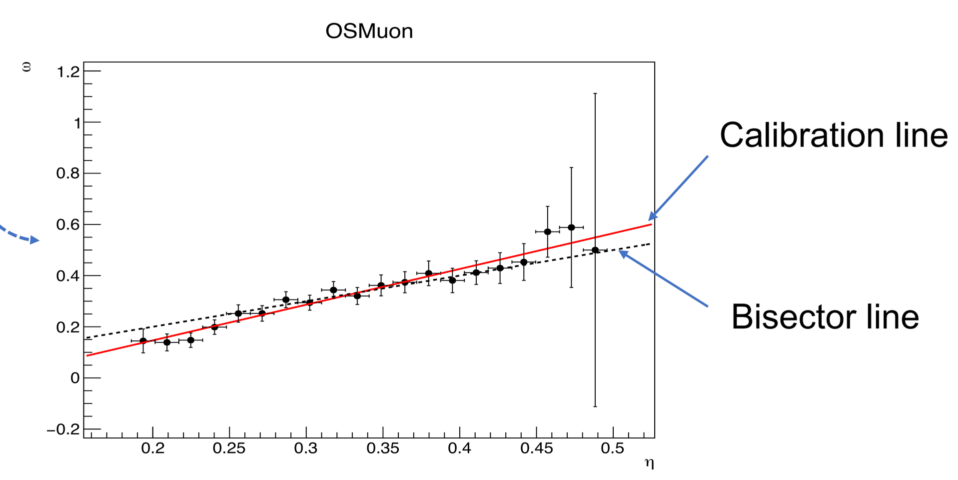
Same-side (SS) and opposite-side (OS) tagging algorithms are used.



Working principle of same-side (SS) and opposite-side (OS) tagger algorithms at LHCb.

Tagging algorithms are trained with self-tagging modes. The response on $B^0 \to K^+K^-K_S$ needs to be recalibrated using MC information or self-tagging modes with similar topology to the signal.

The typical **tagging power is** ~5% at LHCb.



$$\omega = \frac{wrong_{tag}}{wrong_{tag} + right_{tag}}$$

Calibration of the OSMuon tagger using MC truth information: the estimated mistag probability η by the tagger is compared to ω.

State of art of the analysis: data selection

Data and MC Ntuples have been recreated for Run1 and Run2 samples, using the **LHCb DaVinci software:**

- Flavour-tagging information included.
- Comparison with Ntuples used for branching-fraction analysis.

The selection of data and MC samples involves several steps:

- Reconstruction.
- Stripping: preliminary loose cuts.
- Trigger: hardware and software.
- Preselection: based on kinematic and geometric variables.
- Vetoes of decays that proceed through charm or charmonium intermediate states: D^0, $D^\pm$, $D_s^\pm$, $\Lambda_c^\pm$, J/ψ, χ_{c0}.
- MVA selection: Multivariate Analysis response based on topological and particle-identification (PID) variables to reduce crossfeeds.

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