Decay Chain Reconstruction in Belle II.

Francesco Tenchini* (DESY), Jo-Frederik Krohn (Univ. of Melbourne) (on behalf of the Belle II Software Group)

*francesco.tenchini@desy.de



The Belle II Experiment

The Belle II experiment [1] aims to exploit the asymmetric e+e-collider SuperKEKB at KEK, Japan, designed to provide an instantaneous luminosity of 8x10³⁵ cm⁻²s⁻¹ at the Y(4S) mass resonance.

The goal is a total data sample of 50 ab⁻¹, two orders of magnitude larger than in first generation B Factories KEKB and PEP-II.

The asymmetric beam design boosts collision products along the beam axis, increasing their flight lengths in the lab frame and facilitating the study of timedependent CP violating processes.

Precise decay point reconstruction is a lynchpin of these studies, as well as an essential tool for background rejection and enhancing the size of the useable physics sample.

Vertex Fitting

Vertex fitting techniques see widespread use in particle physics.

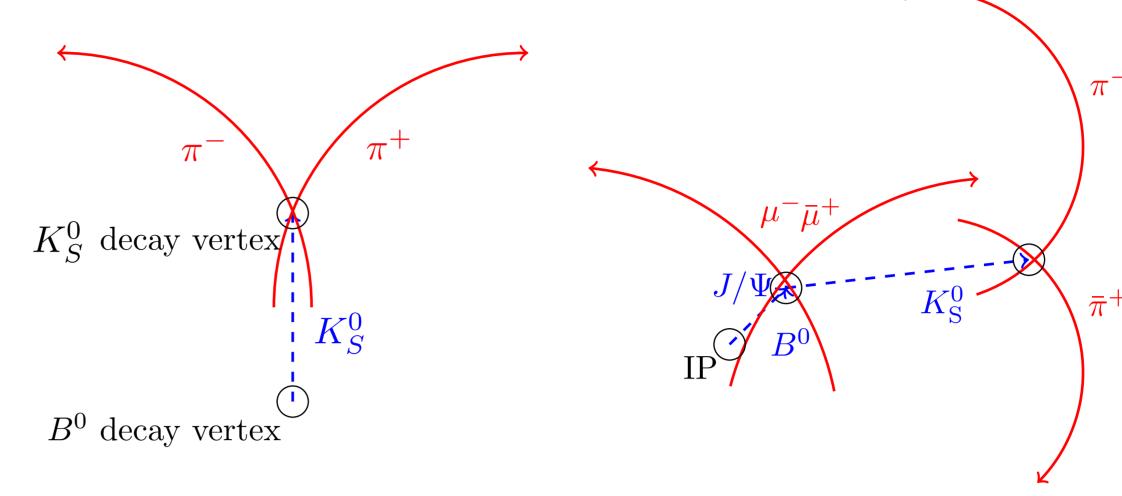
Use cases include:

- Precision measurements of decay vertex positions;
- Combinatorial background rejection;
- Improving particle mass and momentum resolution;
- Indirect detection of resonant states.

The Belle II analysis software framework (basf2) provides several vertex fitting tools, such as:

- KFit, based on a least square minimisation, developed for Belle [2].
- RAVE, a standalone package originating from the CMS libraries [3].
- TreeFitter, a tool based on a global approach, originally developed in BaBar [4].

Approaches to Decay Chain Reconstruction



Charged tracks in a magnetic field fit to a common decay vertex.

Complex decay chain, comprising several individual vertices.

Leaf-by-leaf approach to decay chain reconstruction:

This is the simplest approach. Vertices in the chain are reconstructed individually; In the example we first reconstruct $K_s \rightarrow \pi^+\pi^-$ and $J/\psi \rightarrow \mu^+\mu^-$, then $B^0 \rightarrow J/\psi$ K_s. The fit is blind to information two or more stages down in the chain.

Global approach:

The full tree is parametrised and fitted simultaneously. Challenging, but allows treatment of hard to fit processes such as those involving neutral particles. The full covariance matrix of all the observables is available to the user.

Global Fit Implementation

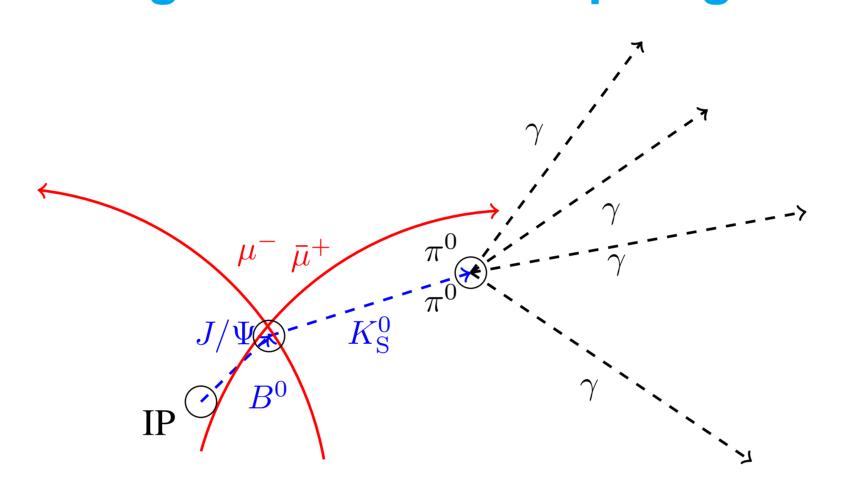
The computational challenge of a global approach lies in the inversion of large matrices.

A particle in the decay chain can have up to seven free parameters $(E, p_x, p_y, p_z, x, y, z)$ rapidly making a naive least square approach unfeasible as the decay complexity increases.

We implement a twofold solution:

- We use a Kalman Filter [5] approach to the minimisation. In this method, fit constraints are applied one by one iteratively to a subset of the state vector, replacing the inversion of a large matrix with a series of smaller matrix operations.
- We rely on the the EIGEN library [6] for fast treatment of matrix operations. This significantly improves execution speed compared to other libraries in use by basf2.

Fitting Neutral-Rich Topologies



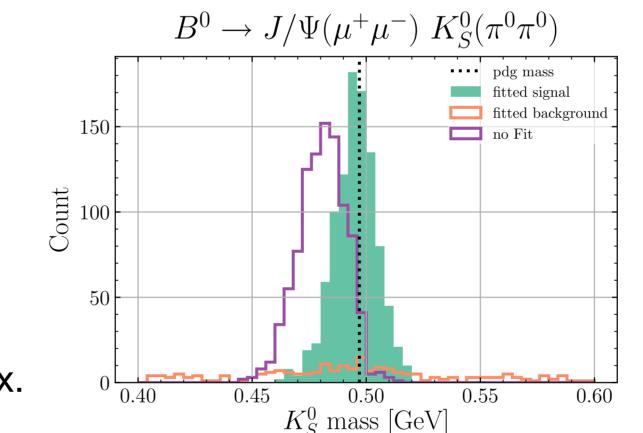
A global approach is able to correct this bias by using information from the rest of the decay chain.

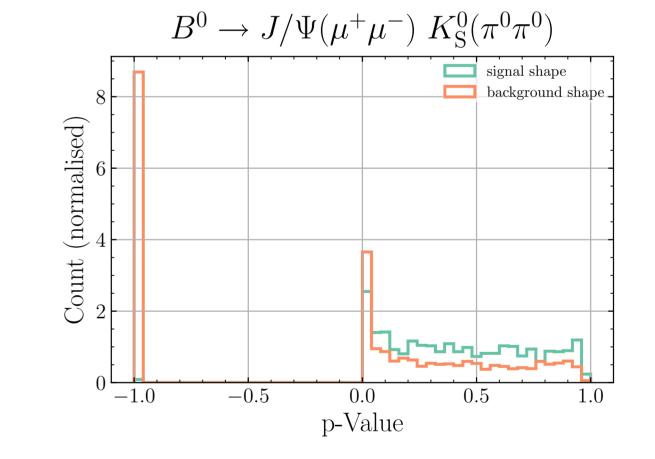
In this example using simulated data, the B⁰ \rightarrow J/ ψ K_s(π ⁰ π ⁰) decay chain is fitted by applying a mass constraint on the π^0 and using information from the J/ψ vertex.

The K_s mass bias present in the unfitted sample is corrected and the resolution is improved. A mass selection could then allow for the separation of combinatorial background.

Neutral particles do not have associated tracks and are only identified by their energy deposit in the Belle II calorimeter. Therefore, their true momentum vector is unknown; reconstruction assumes it to originate from the interaction point.

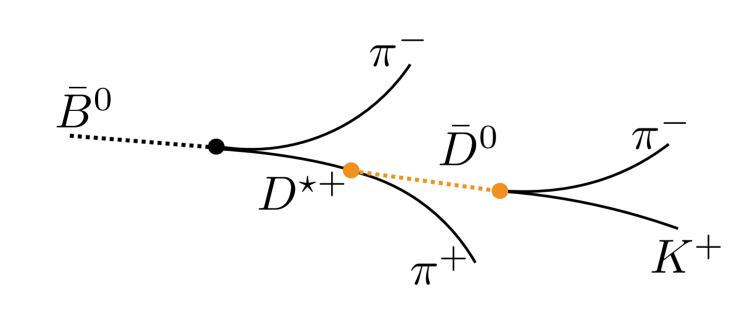
This introduces significant systematics in the case of a displaced, neutral rich vertex.





 \bar{D}^0

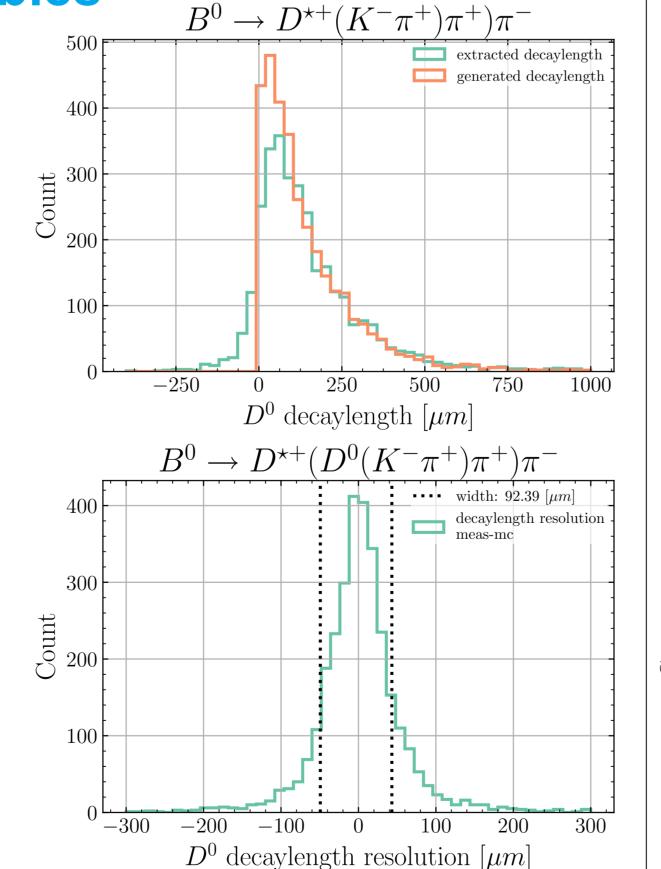
Direct Extraction of Observables



TreeFitter allows for decay chain quantities to be parametrised in a simple manner and saved as output for physics analysis.

The global approach provides access to the full decay covariance matrix, allowing straightforward and consistent treatment of errors.

In this example from a simulated sample, the $\overline{B}^0 \rightarrow D^{*+}(\overline{D}^0(K^+\pi^-)\pi^+)\pi^-$ decay chain is fitted to extract the D⁰ decay length.

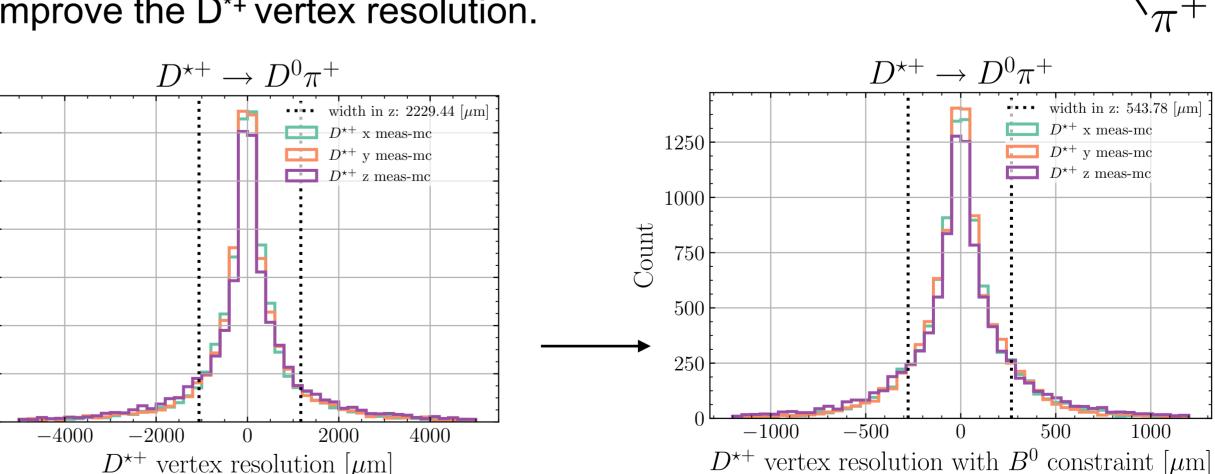


Custom Constraints

 $D^{\star+}$ vertex resolution $[\mu m]$

TreeFitter is designed to allow a variety of personalised constraints to be designed and implemented according to the needs of the analyst.

In this example, the $\overline{B}^0 \rightarrow D^{*+} \mu \nu_{\mu}$ decay chain cannot be trivially fit, as the undetected neutrino would introduce too many free parameters. Instead, the \overline{B}^0 origin vertex is constrained to a previously measured distribution to improve the D*+ vertex resolution.



References

[1] T. Abe et al. [Belle-II Collaboration], arXiv:1011.0352 [physics.ins-det]. [2] J. Tanaka, Belle Note 194. [3] W. Waltenberger, IEEE Trans. Nucl. Sci. 58 (2011) 434.

[4] W. D. Hulsbergen, Nucl. Instrum. Meth. A 552 (2005) 566. [5] R. Fruhwirth, Nucl. Instrum. Meth. A 262 (1987) 444. [6] http://eigen.tuxfamily.org

