



HEP Annual Meeting

Weak Mixing Angle Determination and VELO Upgrade Commissioning

Abbie Jane Chadwick

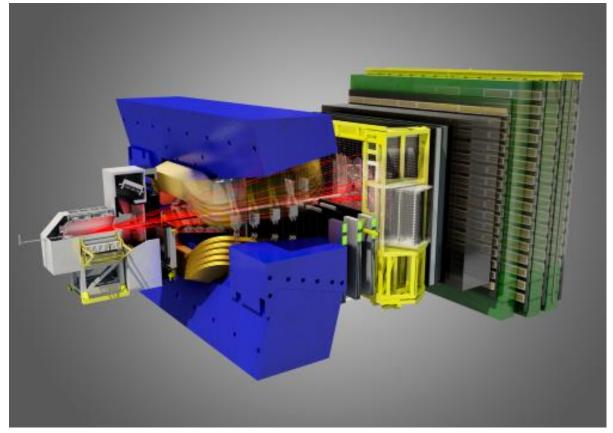
Supervised by Prof. Tara Shears and Dr. David Hutchcroft



My Research Areas

Weak Mixing Angle

- LHCb pseudorapidity range $2~<~\eta~<5$
- he weak mixing angle, $\text{Sin}^2\theta_W$, is a fundamental standard model parameter that relates the W and Z boson masses
- All parameters need to be very well characterised with high precision
- Run 2 data, 6fb⁻¹ via the forward backward asymmetry, A_{FB} in $Z/\gamma^* \rightarrow \mu^+ \mu^-$
- Previous LHCb result used 7 TeV and 8 TeV with 1 fb⁻¹ and 2 fb⁻¹ of data respectively

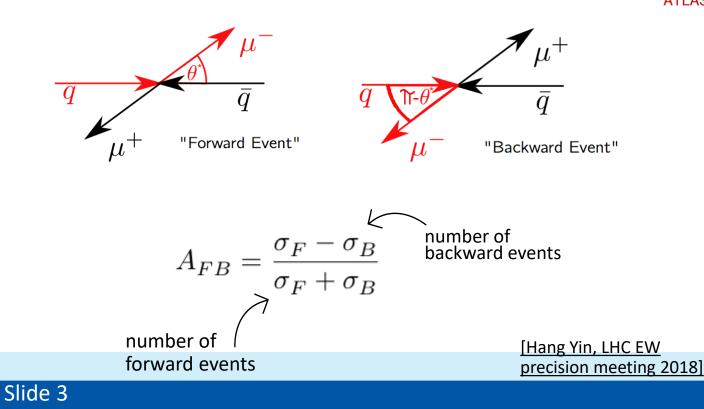


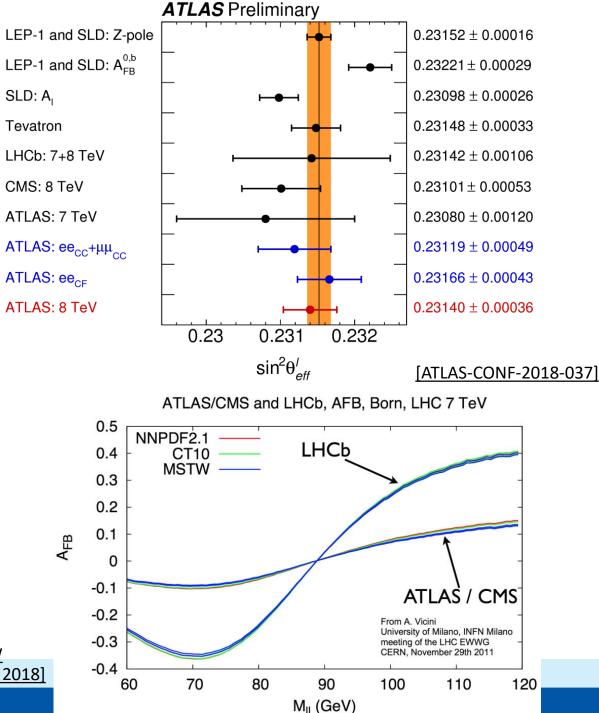
[LHCb - CERN]

 $\sin^2 \theta_w^{eff} = 0.23142 \pm 0.00073 (stat.) \pm 0.00052 (sys.) \pm 0.00056 (theory)$ [2015]

Weak Mixing Angle $Sin^2\theta_W$

- LEP and SLD are the most precise measurements
- 3.2σ variation between those two
- Weak mixing angle cannot be measured directly, it is extracted from the measurement of variables sensitive to it (eg A_{FB})

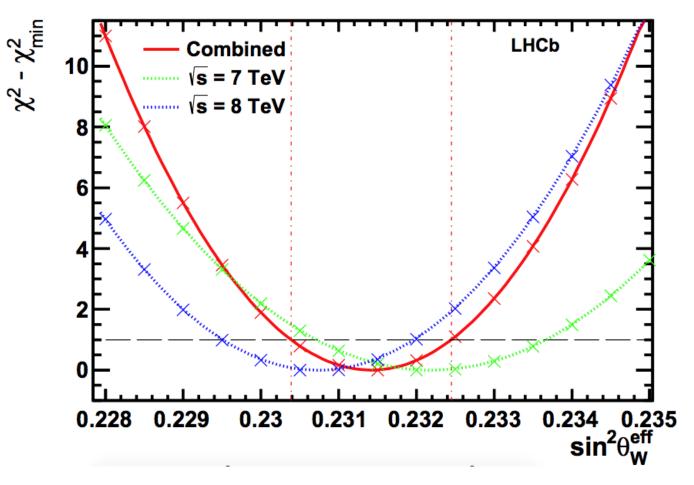




$Sin^2\theta_W$ Calculation at LHCb

- Values for A_{FB}^{pred} are found via MC using a range of values for $sin^2(\theta_W^{eff})$
- χ^2 is calculated by comparing A_{FB}^{pred} to data values of A_{FB}
- Quadratic functions are fitted to the distributions
- The difference between χ^2 values and the minimum χ^2 value is plotted as a function of the $sin^2(\theta_W^{eff})$ values used in MC
- The minimum of the plotted χ^2 distribution is the final value of $sin^2(\theta_W^{eff})$

From the 2015 3fb⁻¹ measurement



[LHCb, 1509.07645]

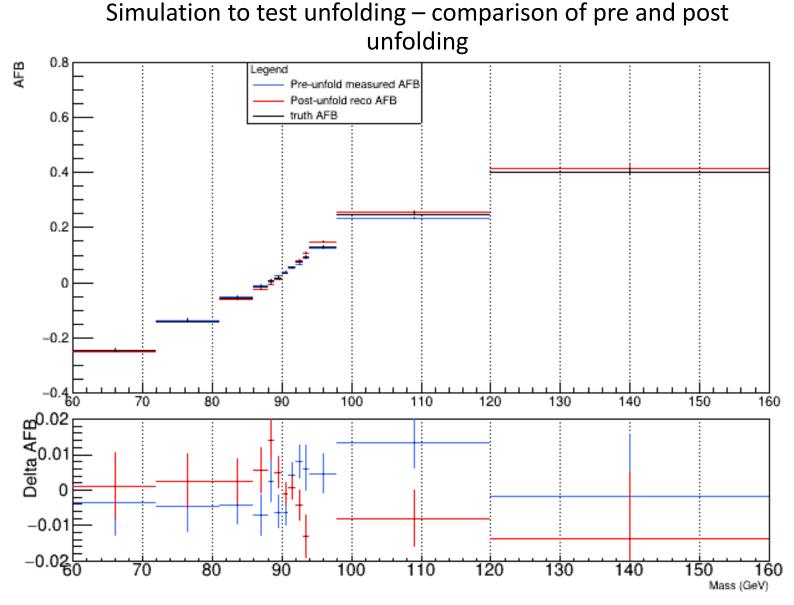
Unfolding Study

Many steps to get the weak mixing angle measurement including:

• Unfolding

Unfolding removes the effect of measurement resolution, systematic biases and detector efficiency to give true AFB values

- Backgrounds
- Extract results
- Systematic errors



1D unfolding in Z mass

Unfolding Study Conclusion

0.6

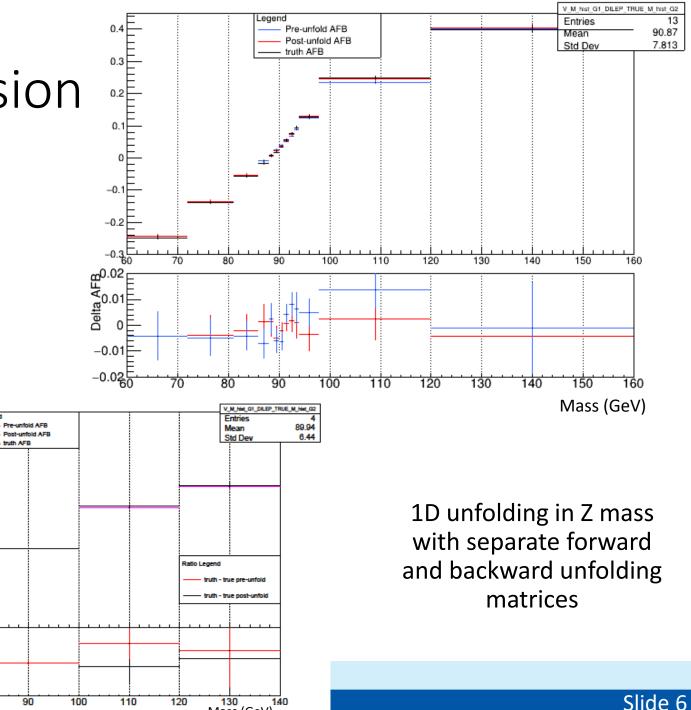
-0.2

-0.02

70

80

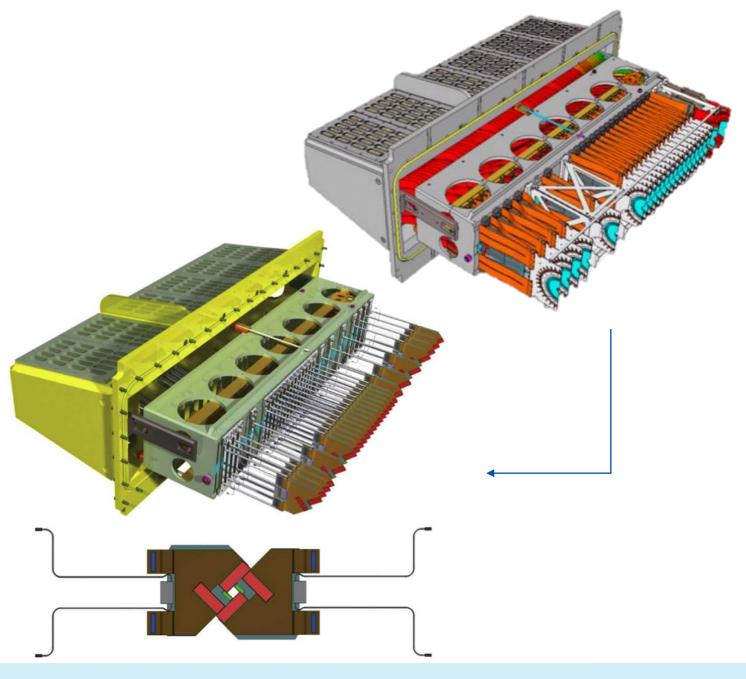
- Using split forward and backward unfolding matrices removes most of the step in the unfolded data around 90GeV
- A variety of binning schemes trialled
- When a course binning scheme is used for unfolding it shows a good agreement
- AFB is still sensitive to $\text{Sin}^2\theta_W$ even with fewer bins



Mass (GeV)

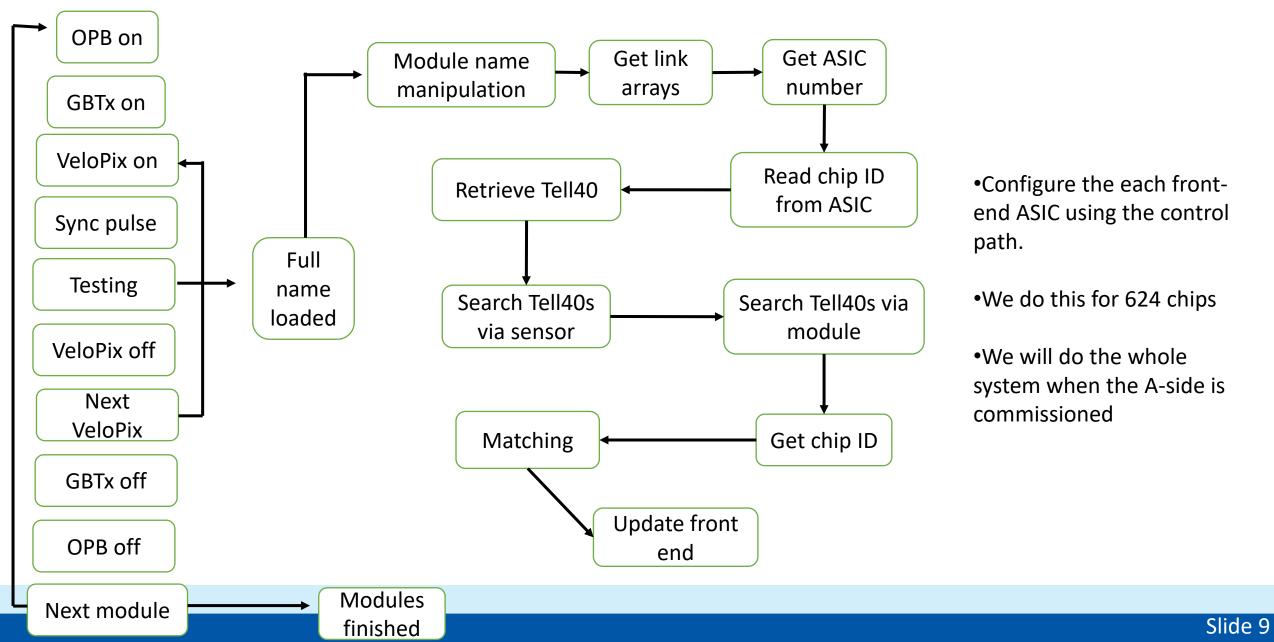
My Research Areas

- VELO is the inner tracking system of LHCb
- Upgraded VELO:
 - 52 hybrid pixel modules
 - 4 sensors per double sided module
 - Each sensor bonded to three VeloPix ASICs
 - 5.1mm away from beam in closed position
 - 40MHz readout



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- WinCC OA
- Cable mapping panel
- Create mappings of crucial elements of VELO
- Check these elements against what is to be expected
- Panels that will be run as part of the testing and running of VELO



Next Steps

Weak Mixing Angle Analysis

- The next step of the analysis is to complete all background studies
 - Semi-leptonic heavy flavour decays
 - Hadron misidentification
 - Electroweak and top production
- Systematics will then be started

- Testing on the full system once A side is commissioned
- Panel then ready for use during runs
- Noise scan panel



Also:



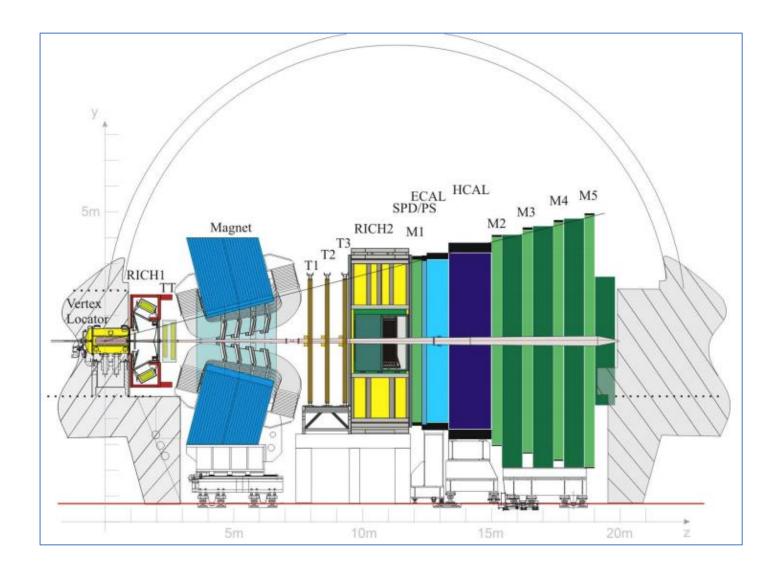
- Outreach
 - Co-ran a year 12 particle summer school online in August 2021
 - Helping to organise the 2022 school
 - Interviewed for The Institute for Research in Schools (IRIS)
- Applied for the Bell Burnell Graduate Scholarship Fund to extend my funding
- Currently on LTA at CERN until October 2022
- Thesis writing has begun!



Backup Slides

The LHCb Experiment

- Single-arm forward detector which has forward angular coverage of 15-300 mrad (bending plane/horizontal plane) and 15-250 mrad (non-bending plane/vertical plane) [1]
- At high energies $b\overline{b}$ pairs are produced with a strong boost along the beam line
- During run I (2010-2012) and run II (2015-2018) took 9 fb⁻¹ worth of data (3-6 split)
- Instantaneous luminosity of 4 x 10³² cm⁻²s⁻¹

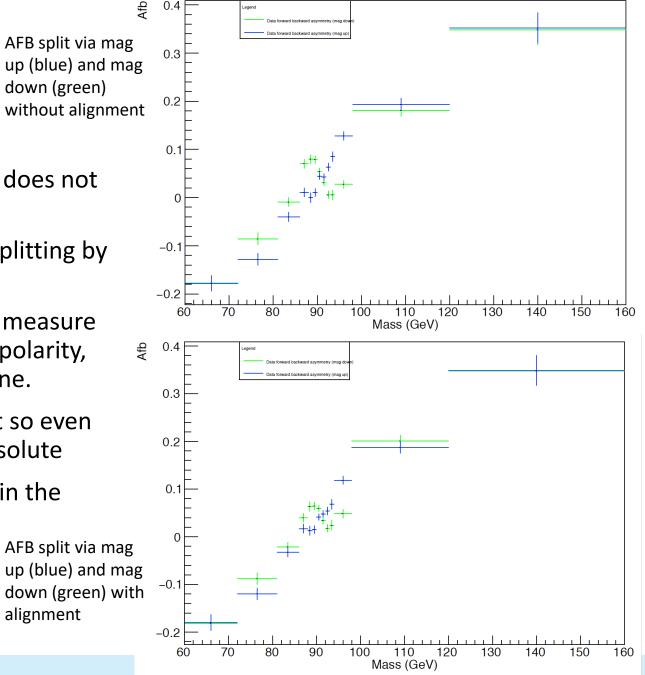


Alignment Study

AFB split via mag up (blue) and mag down (green)

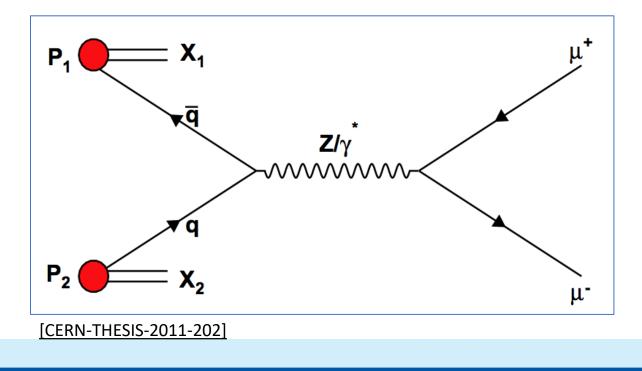
alignment

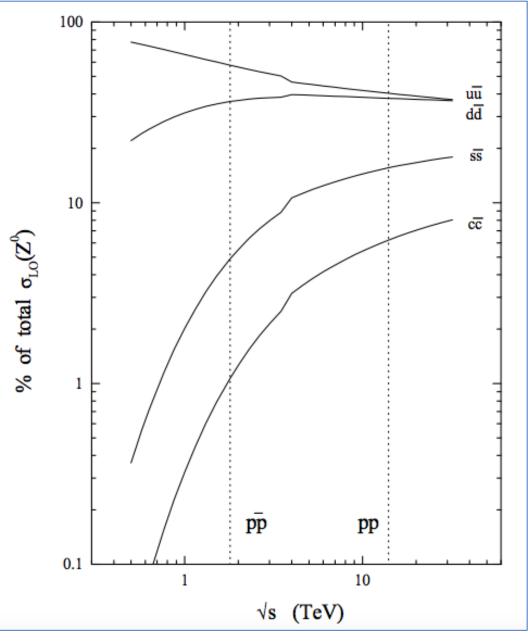
- There is a bump around the Z mass region which does not match MC
- This was investigated and the issue arose when splitting by ٠ polarity
- To correct for changes in the detector's ability to measure charge and momentum of particles according to polarity, an alignment can implemented - in this case offline.
- A_{FB} is sensitive to imperfections in the alignment so even though an improvement can be seen, it is not absolute
- The residual that is left can be corrected for within the ٠ unfolding



Z Production at the LHC: Drell-Yan Process

- Quark-antiquark (same flavour) annihilation to produce a virtual photon γ*/Z boson
- Decays into a lepton pair

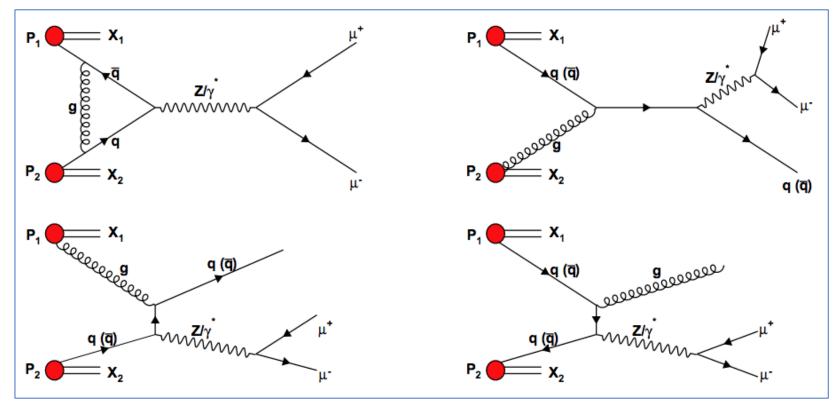




[Phys. J. C, 14:133-145, 2000]

Drell-Yan Process

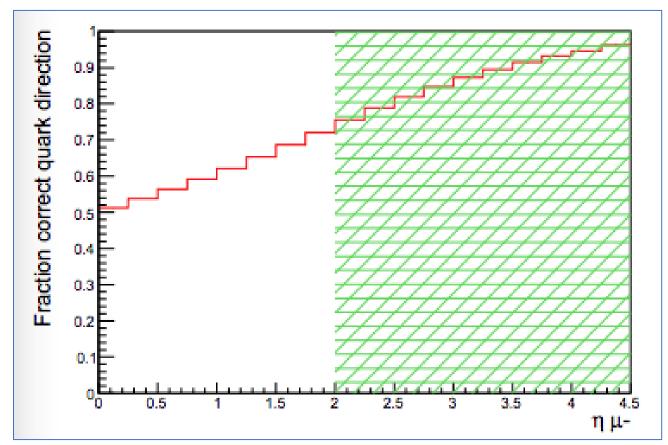
- A quark can be either valence or a sea quark, an antiquark can only be a sea quark (pp collisions)
- Higher order Feynman diagrams for the Drell-Yan process on the right
- Z and γ mixing produces a differential cross section that is a combination of three contributions: Z, γ and another dependant on both
- There is a cosθ dependence within a term which produces an asymmetry



[CERN-THESIS-2011-202]

LHCb and Weak Mixing Angle $Sin^2\theta_W$

- LHCb focuses on higher rapidity range, $2 < \eta < 5$, which has high sensitivity to A_{FB} and therefore $Sin^2 \Theta_W^{eff}$
- Asymmetry most pronounced when the Z boson direction is correctly known
- The further forward the more likely that the Z boson follows the direction of the quark
- LHCb focuses on the forward region and the further forward in rapidity, the more likely the Z forward direction is determined correctly



[LHCb-ANA-2015-002 28/09/2015]

Unfolding

- Response matrix is filled by looping over a training sample containing known measured and truth data
- Response matrix gives the fraction of events from the true distribution that are ultimately within corresponding the measured distribution bin
- This is then used via RooUnfold implementation on measured data of choice to find unknown truth

- There are many unfolding algorithms within RooUnfold:
 - Bayesian unfolding currently used
- 1D, 2D and 3D unfolding possible

Forward Backward Asymmetry, A_{FB}

