

# Using the HFAG fit for $\tau_S$

Encoder: Ken Hayes

Overseer: Klaus Mönig

LBNL resp.: Juerg Beringer

# Present situation

- The  $\tau$ -branching ratios are obtained from a constrained fit to all data
- All decay modes are broken down into basis modes which are constrained to add up to 1
- At the moment we use the standard PDG fit with the standard algorithm for error scaling
- Correlations inside the measurements of a given publication can be taken into account if the publication contains the correlation matrix
- At present we miss decay modes with a sum of 0.08% in the fit
- The best measured decay modes have a relative error of 0.2%
- An update of the fit is desirable, but not absolutely necessary

# A note on error scaling

- The fit scales errors of several modes with a CL of 10-15%
- Without scaling the final  $\chi^2/\text{ndf}$  is 129/109 (prob=9%)
- We know there is a problem in the  $\pi\pi K$ ,  $\pi KK$ ,  $KKK$  modes which contribute a  $\chi^2$  of  $\sim 40$  for 14 measurements
- If one subtracts the excess  $\chi^2$  ( $\sim 25$ ) the final  $\chi^2$  is perfect
- This indicates that no scaling apart from these modes is needed, confirmed by the individual ideograms for the other modes which are scaled

# The HFAG fit

- The Heavy Flavour Averaging Group also performs a full fit to the  $\tau$  branching ratios
- Their fit is also able to take common systematics between different publications into account
- The fit contains no automatic error scaling but the scaling for the problematic 3h modes has been introduced
- If error scaling and common systematics are switch off in the PDG and the HFAG fit both fits agree perfectly

# Proposal to use HFAG fit

We propose to use the HFAG fit for the PDG averages

- External fits are used successfully already in the PDG, e.g. the Z properties
- The HFAG fit is supported by the chair of the HFAG  $\tau$ -group, A. Lusiani, who has a permanent position in Pisa
- The group is willing to provide fits to us on a regular basis using exactly the data we use in our listings
- Their fit should give more reliable results due to the better treatment of common systematics
- Not to duplicate the work we should discuss the inclusion of more basic modes only after we decided which fit to use