

# Ionization matrix element retrieval & MF reconstruction from alignment traces

## N<sub>2</sub> Results Summary

22nd Oct. 2016

**Summary document (Oct. 2017), for full details see:**

Bootstrapping to the Molecular Frame with Time-domain Photoionization Interferometry  
Marceau et. al. (2017)

Data and documents: <https://doi.org/10.6084/m9.figshare.4480349>

arXiv: <https://arxiv.org/abs/1701.08432>

Original experiments, data & data analysis: Claude Marceau

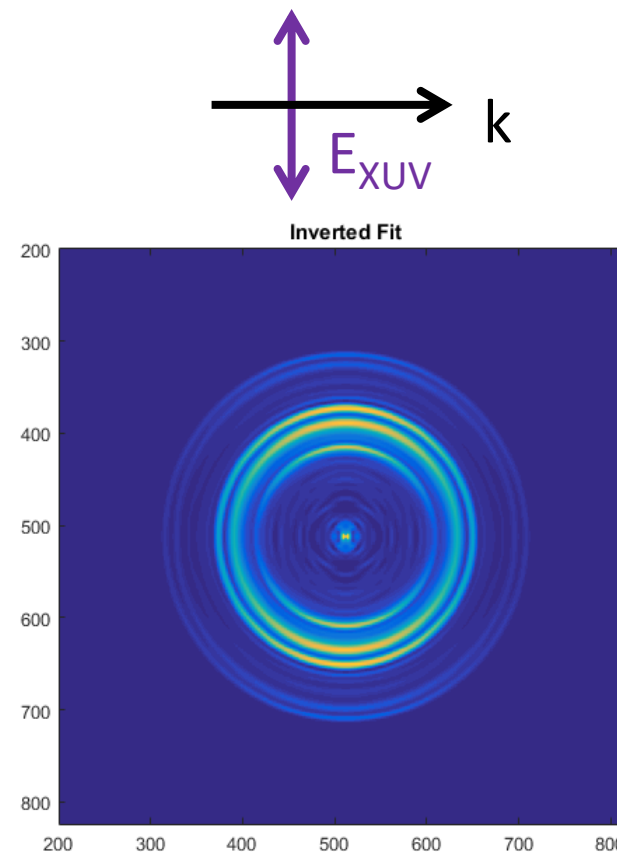
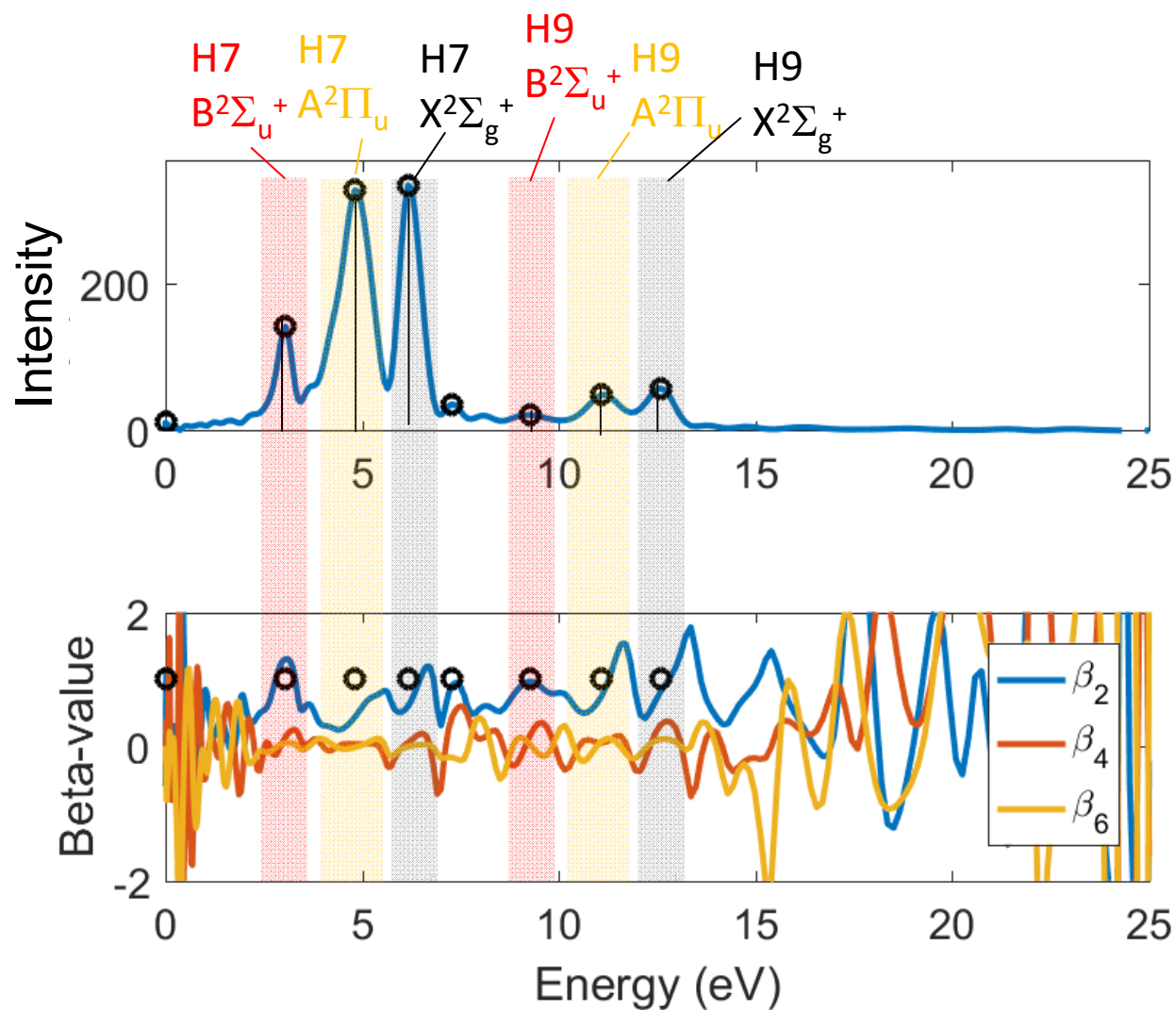
Alignment trace calculation & fitting: Varun Makhija

Photoionization calculation & fitting: Paul Hockett

### Aims

- VMI with XUV
- Molecular alignment
- Determining the alignment
- Extracting the dipole matrix elements
- Reconstructing the molecular frame

# N<sub>2</sub> - Abel inversion results



## Varun's fitting (determining the alignment)

### Notes from Varun's thesis

Laser-induced rotational dynamics as a route to molecular frame measurements

<http://krex.k-state.edu/dspace/handle/2097/18522>

where  $\chi$  becomes the azimuthal angle of the laser polarization vector. Since the Wigner functions  $D_{m,k}^j(\theta, \phi, \chi)$  are an irreducible representation on the rotation group  $SO(3)$ <sup>52</sup> the angle dependent ion yield can be expanded as

$$S(\theta, \chi) = \sum_{j,k} C_{j,k} D_{0,k}^j(\theta, \chi), \quad (5.1)$$

$$S(\theta, \chi) = \frac{dW}{d\hat{\Omega}} = \sum_{j,k} C_{j,k} D_{0,k}^j(\theta, \chi),$$

$$C_{j,k} = \sum_{l,m,\lambda,\lambda'} \langle l, -m; l, m | j, 0 \rangle \langle l, -\lambda; l, \lambda' | j, k \rangle A_{l,\lambda} A_{l,\lambda'} d_{l,m}, \quad (5.5)$$

$$S(t) = \int \rho(\theta, \chi, t) S(\theta, \chi) \sin \theta d\theta d\chi = \sum_{jk} C_{j,k} \int \rho(\theta, \chi, t) D_{0k}^j \sin \theta d\theta d\chi = \sum_{jk} C_{j,k} \langle D_{0k}^j \rangle(t). \quad (5.7)$$

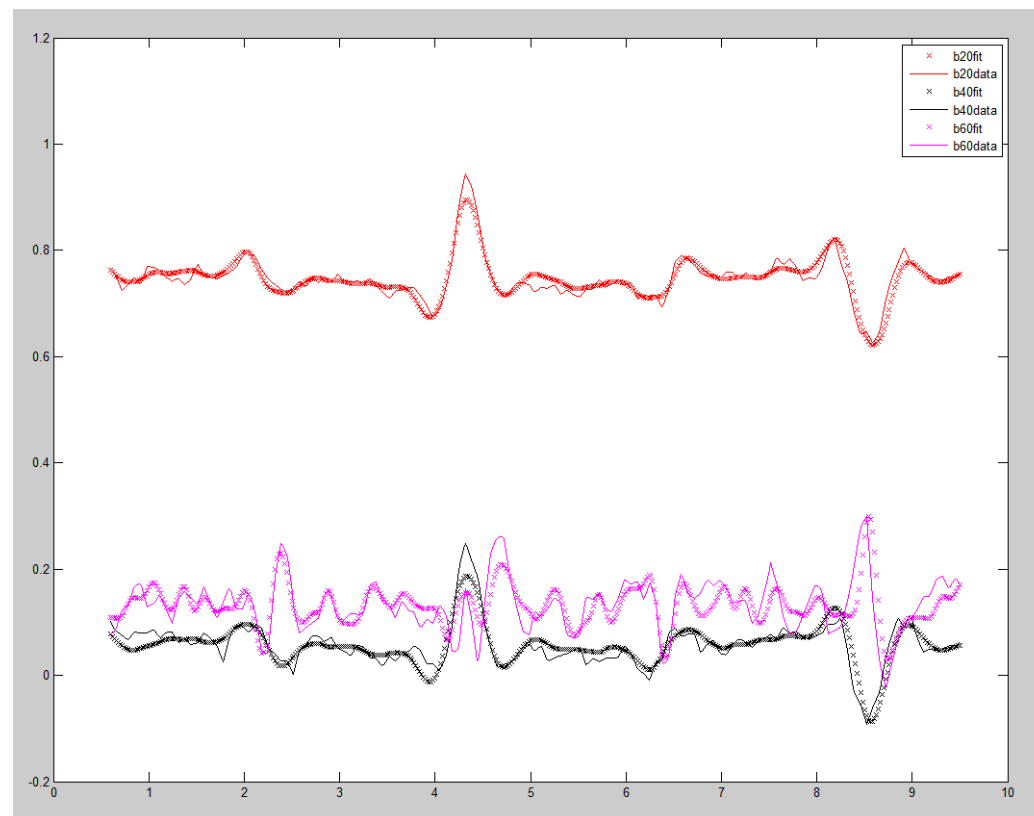
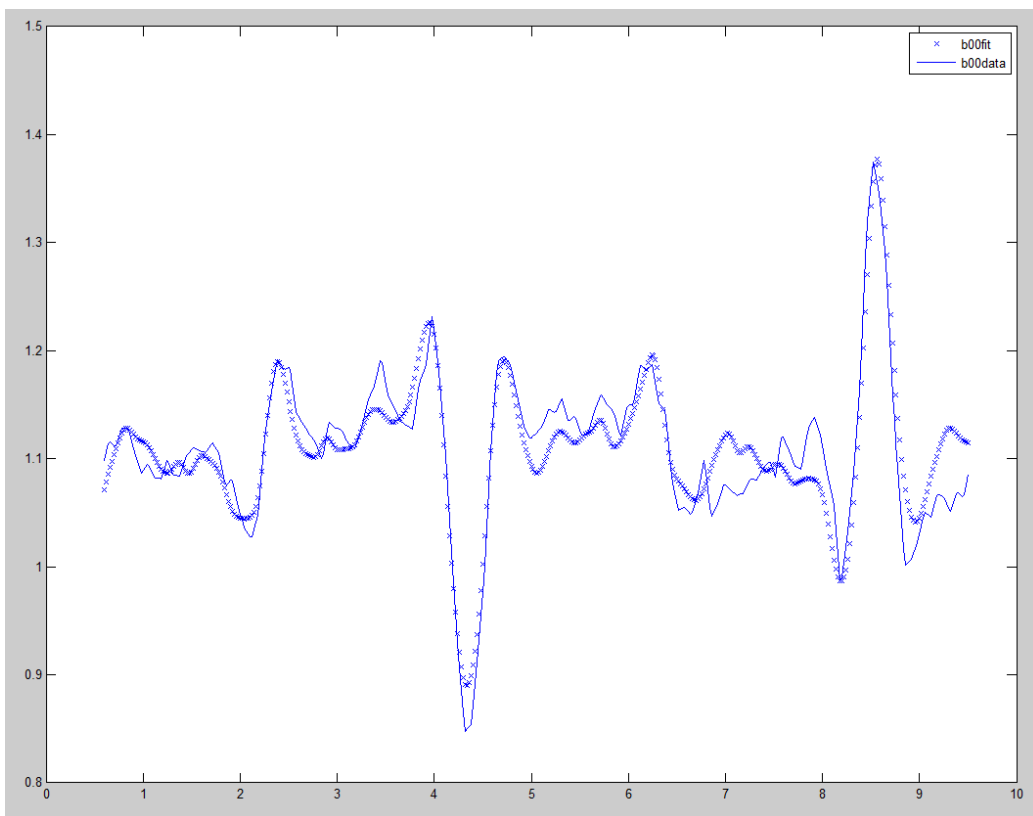
Measured time-dependent signal

Fitted

Calculated from rotational wavepacket simulations  
Function of laser parameters & rotational temperature

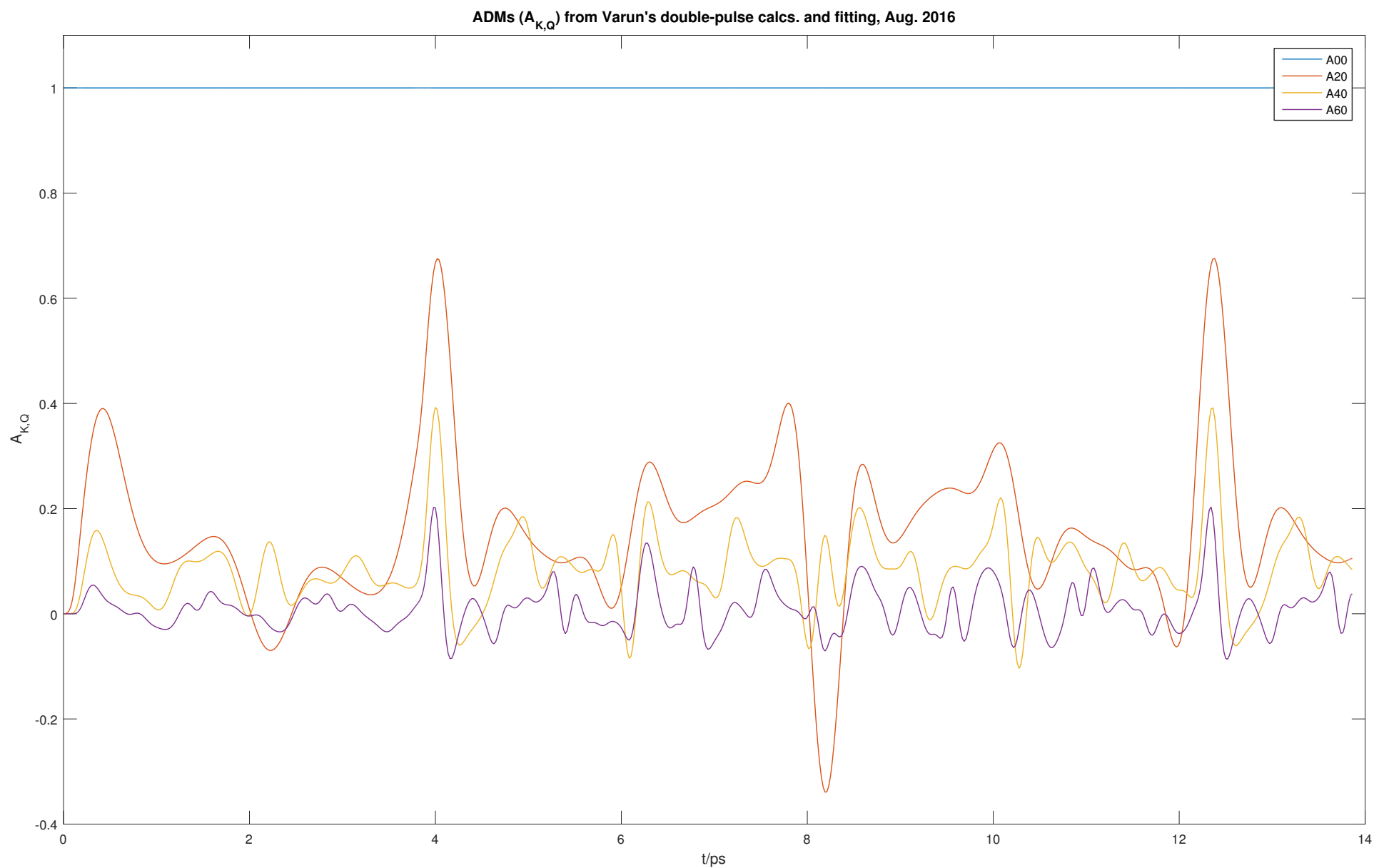
## Varun's fitting (determining the alignment)

Data - double-pulse alignment data, X-state H5



## Varun's fitting (determining the alignment)

The alignment is characterised by axis distribution moments (ADMs) defining the alignment in terms of spherical harmonic expansion coefficients.



## Paul's fitting (determining the photoionization dynamics)

Use known ADMs to determine the unknown dipole matrix elements. Everything else is angular momentum coupling and symmetry parameters; complicated, but analytical.

$$\begin{aligned}
 \beta_{L,M}(t) &= (2L + 1)^{1/2} \sum_P (-1)^P \begin{pmatrix} 1 & 1 & P \\ p & -p & R \end{pmatrix} e_{-p} e_{-p}^* \\
 &\times \sum_K \sum_Q (2K + 1)^{1/2} \begin{pmatrix} P & K & L \\ Q - M & -Q & M \end{pmatrix} A_{K,-Q}(t) \\
 &\times \sum_{q,q'} (-1)_{q'} \begin{pmatrix} 1 & 1 & P \\ q & -q' & q' - q \end{pmatrix} \begin{pmatrix} P & K & L \\ q - q' & q' - q & 0 \end{pmatrix} \\
 &\times \sum_{l,l'} \sum_{\lambda,\lambda'} (-1)^{\lambda'} (2l + 1)^{1/2} (2l' + 1)^{1/2} \begin{pmatrix} l & l' & L \\ \lambda & -\lambda' & M \end{pmatrix} \begin{pmatrix} l & l' & L \\ 0 & 0 & 0 \end{pmatrix} \\
 &\times (-i)^{l'-l} \sum_{\Gamma,\Gamma'} \sum_{\mu,\mu'} \sum_{h,h'} b_{hl\lambda}^{\Gamma\mu*} b_{h'l'\lambda'}^{\Gamma'\mu'} \mathbf{D}_{hl}^{\Gamma\mu*}(q) \mathbf{D}_{h'l'}^{\Gamma'\mu'}(q').
 \end{aligned}$$

Measured angular parameters

ADMs from Varun's fit

Matrix elements to determine

See *General phenomenology of ionization from aligned molecular ensembles* (Hockett, NJP, 17 023069 2015) for details.

## **Paul's fitting (determining the photoionization dynamics)**

Inputs:

Data - Claude's updated analysis August 2016

Alignment calculations - from Varun's analysis, 29th August 2016, as per above details.

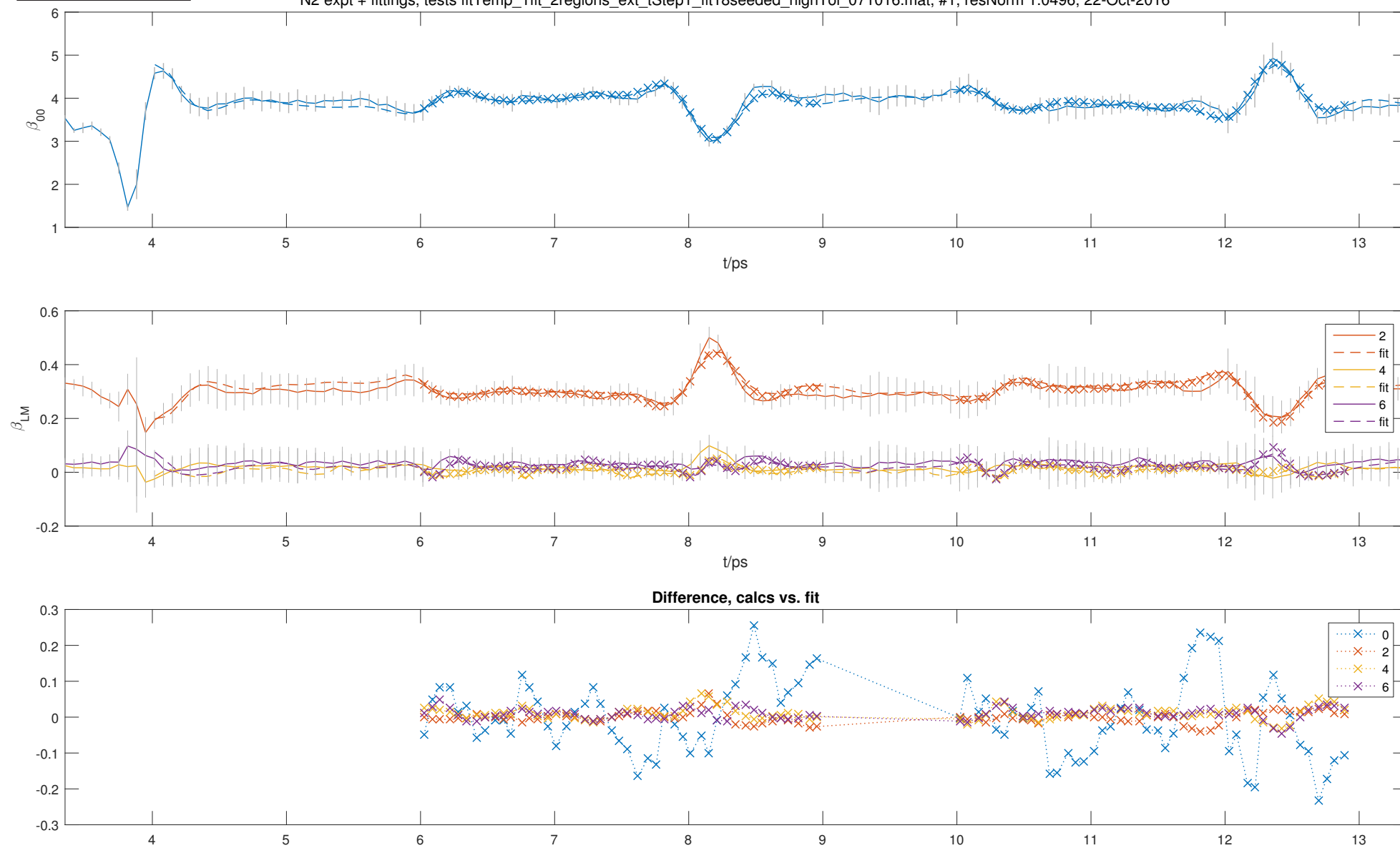
Basic method:

- Renormalize beta values (from Legendre polynomial to spherical harmonic expansion)
- Fitting to determine symmetrized matrix elements
- Statistical sampling of fitting hyperspace via multiple coarse fits with random start vectors (approx. 1 hour per fit)
- Bootstrapping fits via gradually adding additional data points and/or tightening tolerances (multiple hours per fit)

## X-state, H5

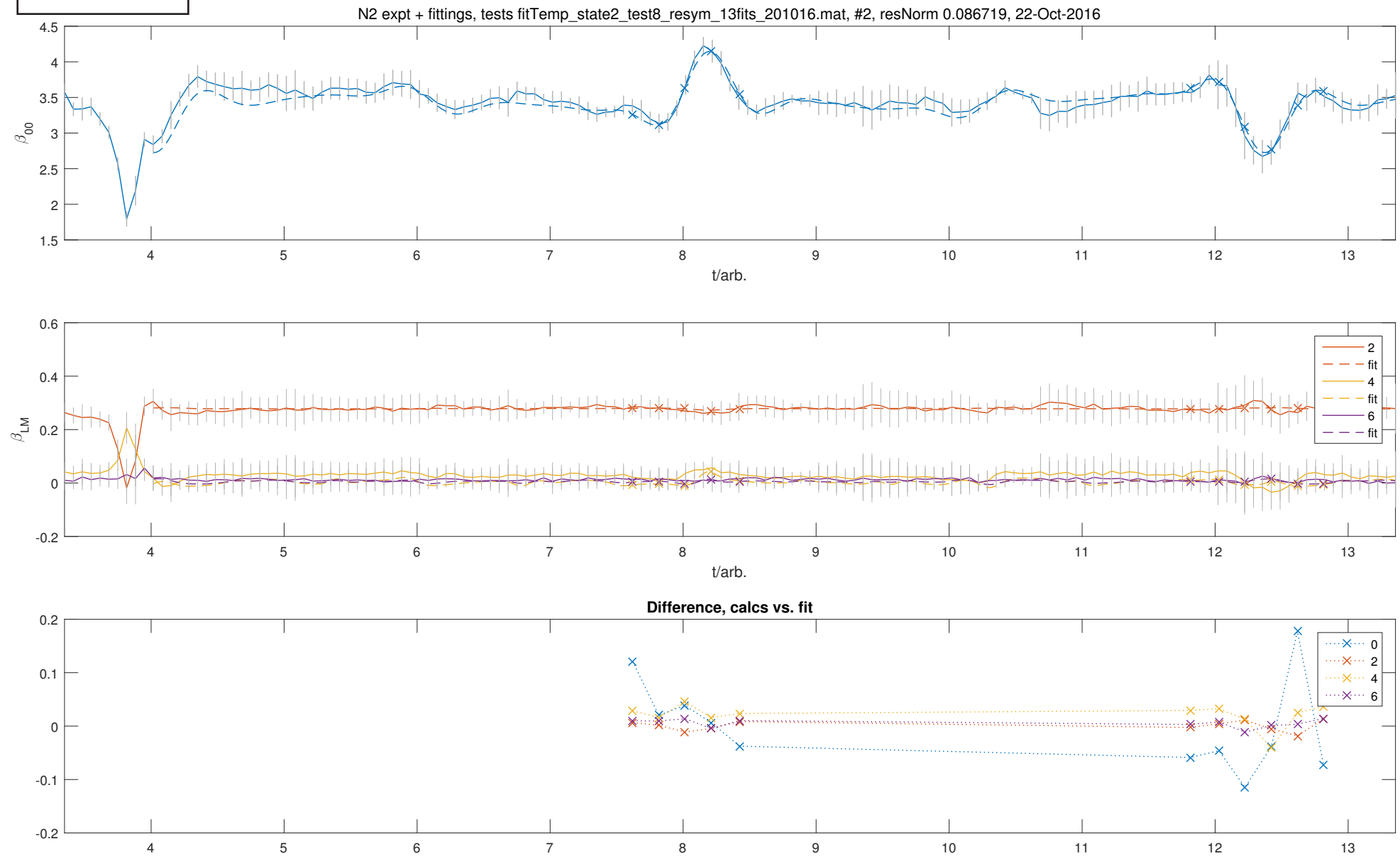
Example results, 'x' marks points included in the fitting  
Experimental uncertainties may be incorrectly renormalised here!

N2 expt + fittings, tests fitTemp\_1fit\_2regions\_ext\_tStep1\_fit18seeded\_highTol\_071016.mat, #1, resNorm 1.0496, 22-Oct-2016



## A-state, H5

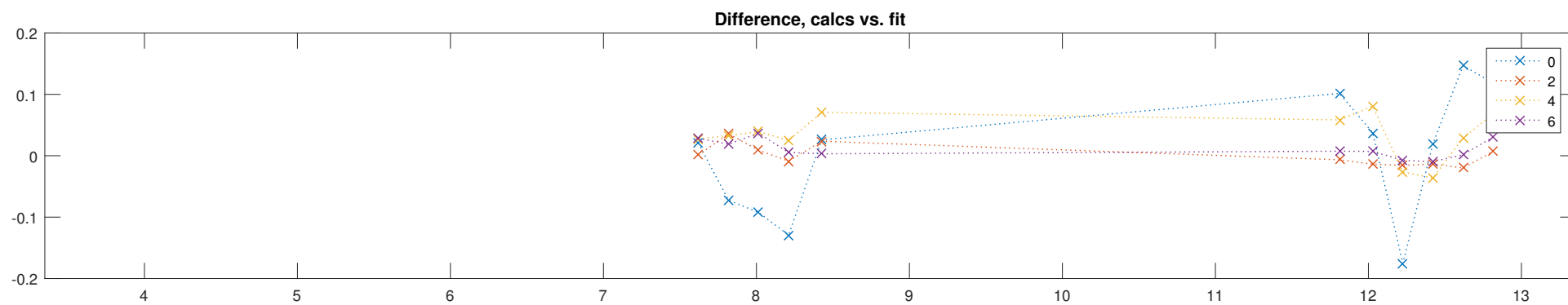
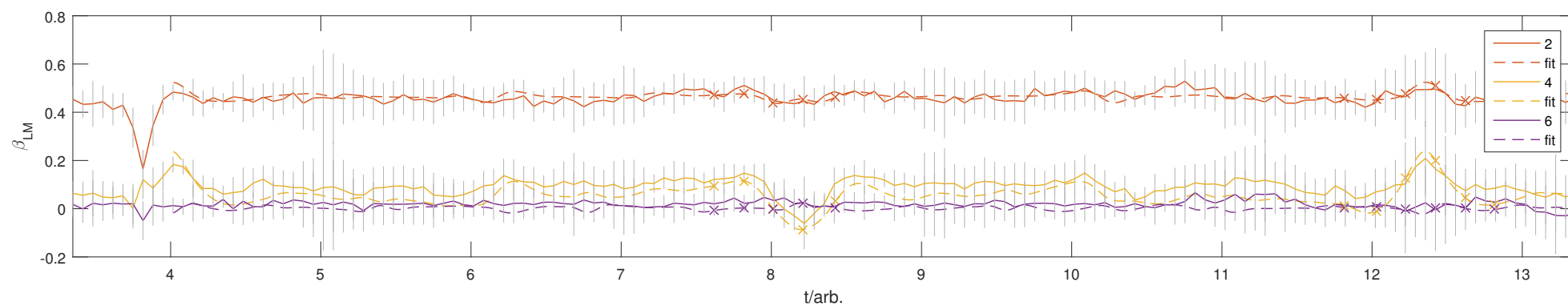
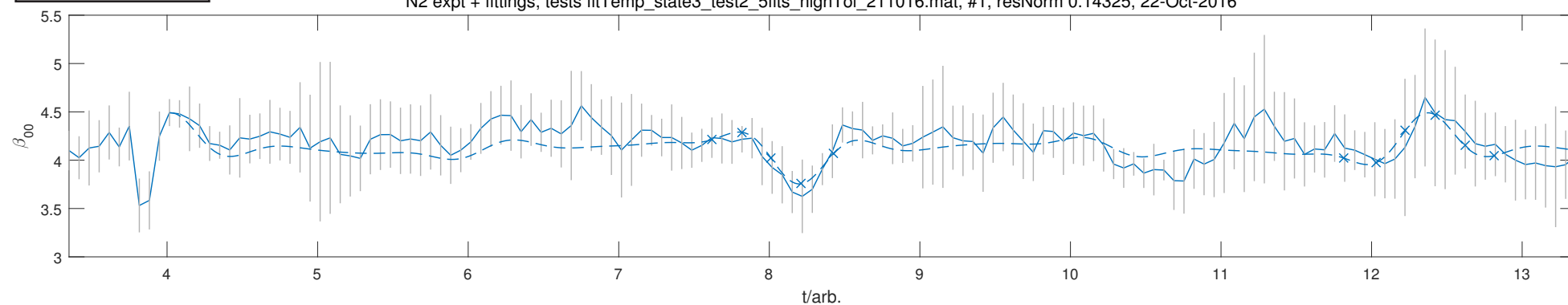
Example results, 'x' marks points included in the fitting  
Experimental uncertainties may be incorrectly renormalised here!



## B-state, H5

Example results, 'x' marks points included in the fitting  
Experimental uncertainties may be incorrectly renormalised here!

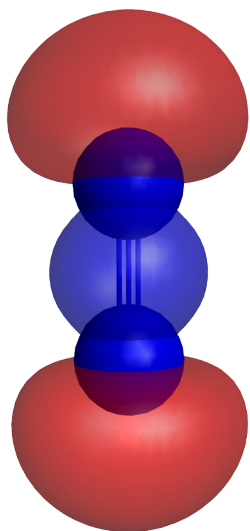
N2 expt + fittings, tests fitTemp\_state3\_test2\_5fits\_highTol\_211016.mat, #1, resNorm 0.14325, 22-Oct-2016



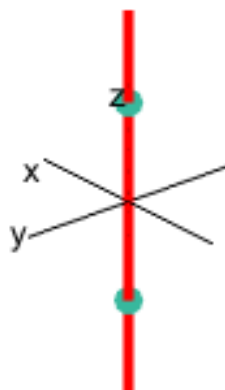
## Molecular frame reconstruction

X-state, H5

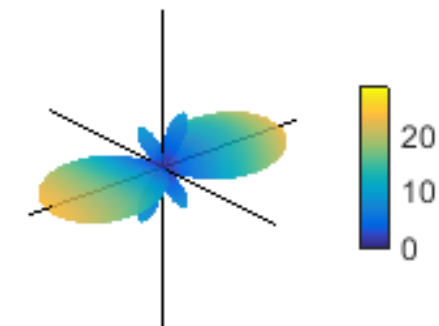
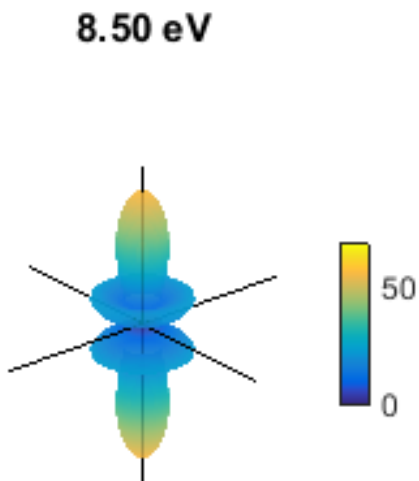
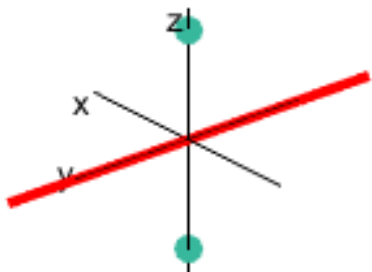
From the matrix elements determined the full MFPAD can be obtained...  
(via another big eqn. similar to the above)



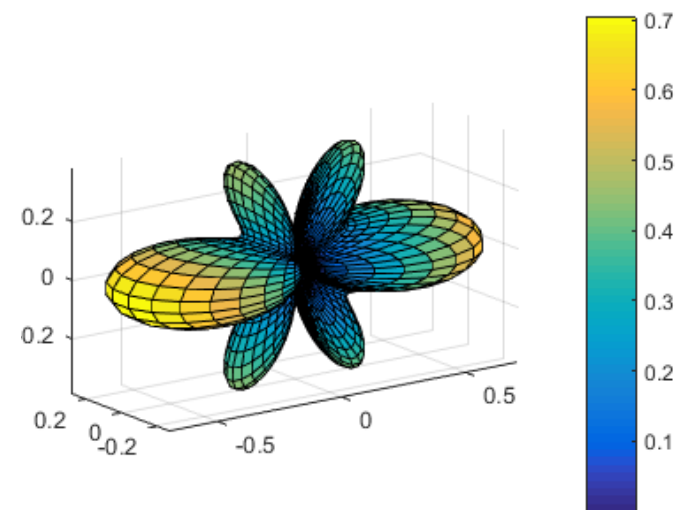
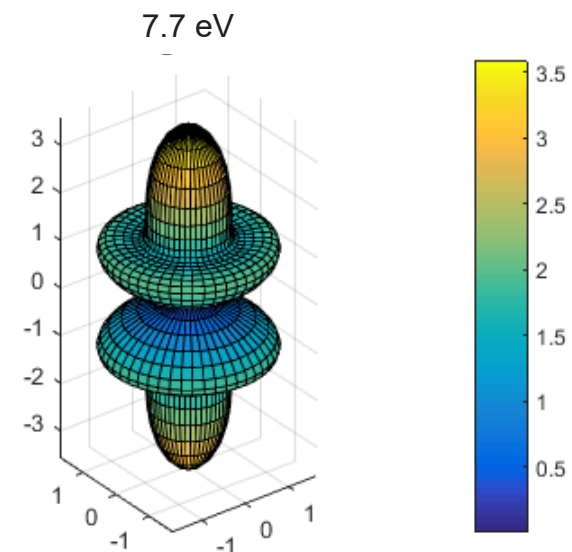
Ionizing orbital  
 $3\sigma_g$



Mol. frame  
polarization geometry



ePS result  
(note energy slightly different)



Determined from fit result

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