Enantiosensitive Structure Determination by Photoelectron Scattering on Single Molecules

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X-ray as well as electron diffraction are powerful tools for structure determination of molecules1-3. Electron diffraction methods yield Ångstrom-resolution even when applied to large systems4 or systems involving weak scatterers such as hydrogen atoms5. For cases in which molecular crystals cannot be obtained or the interaction-free molecular structure is to be addressed, corresponding electron scattering approaches on gas-phase
molecules exist\textsuperscript{6,7}. Such studies on randomly oriented molecules, however, can only provide information on interatomic distances, which is challenging to analyse in case of overlapping distance parameters and they do not reveal the handedness of chiral systems\textsuperscript{8}. Here, we present a novel scheme to obtain information on the structure, handedness and even detailed geometrical features of single molecules in the gas phase. Using a loop-like analysis scheme employing input from ab initio computations on the photoionization process, we are able to deduce the three dimensional molecular structure with sensitivity to the position individual atoms, as e.g. protons. To achieve this, we measure the molecular frame diffraction pattern of core-shell photoelectrons in combination with only two ionic fragments from a molecular Coulomb explosion. Our approach is expected to be suitable for larger molecules, as well, since typical size limitations regarding the structure determination by pure Coulomb explosion imaging are overcome by measuring in addition the photoelectron in coincidence with the ions. As the photoelectron interference pattern captures the molecular structure at the instant of ionization, we anticipate our approach to allow for tracking changes in the molecular structure on a femtosecond time scale by applying a pump-probe scheme in the future.

During the last decade, the determination of the three-dimensional structure of molecules using electron crystallography developed into a complementary analysis method to the well-established X-ray crystallography\textsuperscript{1-3}. In particular, for the structural investigation of micro- and nano-crystalline materials, where sufficiently large single crystals for X-ray diffraction cannot be obtained\textsuperscript{9} or crystalline sponge approaches for X-ray diffraction\textsuperscript{10,11} fail, electron diffraction is the method of choice\textsuperscript{12}.

Pioneering experiments have, in addition, proposed to employ scattering of electrons that were created from within the molecule as a probe. In these experiments, high-energetic single
photons or strong-field laser pulses ionize isolated molecules in the gas phase. The emitted photoelectron is scattered by the molecular potential, yielding a very complex interference pattern, in which the structural information is encoded. Electron diffraction by molecules in the gas phase has been successfully applied for determining molecular constituents\textsuperscript{13}, mapping bond lengths\textsuperscript{14,15} and simple chemical reactions\textsuperscript{16} on ultrafast timescales\textsuperscript{17}. Until now, however, corresponding studies were restricted to linear\textsuperscript{13,16,17} or mostly symmetric molecules\textsuperscript{18-20} such as, e.g., CO, CO\textsubscript{2}, H\textsubscript{2}O, or CH\textsubscript{4}.

Apart from measuring the electron diffraction pattern (in terms of an electron angular emission distribution), the key to electron diffraction experiments on gas-phase molecules is the knowledge of the molecule’s orientation in space\textsuperscript{21}. Molecules in the gas phase are randomly oriented, thus a possible approach is to adsorb the molecule to a surface\textsuperscript{22} or to align the molecule by using laser pulses\textsuperscript{23}. With a single laser pulse, one axis of the molecule can be aligned, which is sufficient only for very small molecules. More complicated, multi-pulse schemes are necessary to orient asymmetric and more complex molecules. Furthermore, reaching a high degree of alignment is challenging\textsuperscript{23}. An alternative approach for detecting the molecule’s spatial orientation is Coulomb explosion imaging\textsuperscript{24}, which, in addition, provides structural information, as well. Here, molecules or molecular ions are rapidly charged up by foil-induced electron stripping\textsuperscript{25}, multiple ionization by a short and strong laser pulse, or by photoionization and subsequent Auger decay\textsuperscript{25}. After the charge-up, the ionic fragments are driven apart rapidly by Coulomb repulsion. Intriguingly, if more than three molecular fragments are generated in the Coulomb explosion, the triple product of three of their momentum vectors allows for identifying whether a chiral molecule was right- or left-handed\textsuperscript{26}. While the absolute configuration of chiral molecules can be determined in principle using this method\textsuperscript{26,27}, it has been restricted, so far, to small molecules with only a few atoms (up to now the largest molecule was halothane with eight atoms\textsuperscript{28}). Gathering structural information of
larger molecules with the help of Coulomb explosion techniques faces multiple challenges. These are, for example, the initial generation of high charge states, the rapidly declining detection efficiency for the coincident detection of many particles\textsuperscript{29}, and uncertainties in the assignment of the different molecular fragments.

In this article, we finally demonstrate in a proof-of-principle study, how to overcome these obstacles. With a combination of the concepts of Coulomb explosion imaging and photoelectron diffraction imaging and support from ab initio modelling it is, indeed, routinely possible even for isolated, mid-sized molecules in the gas phase to determine the full structure of the molecule including its handedness. Our scheme is applicable without the need for advanced laser-alignment schemes or elaborate abilities for detecting a multitude of ionic fragments in coincidence. We will show, furthermore, that our approach allows to determine even detailed of geometrical features, as, for example, a slight displacement of a hydrogen atom in a methyloxirane molecule.

In the present study, we use synchrotron light to ionize the molecule by emission of a core electron. The emerging photoelectron is diffracted by the molecular potential and will be employed as a messenger providing the molecular structure information in its angular emission pattern. Molecules are in most cases unstable after the emission of a core electron. Typically, at least one more electron is released in an Auger decay process and subsequently the molecule fragments into charged and neutral pieces. It turns out, that the detection of the fragmentation direction (i.e., the momentum vectors) of two charged fragments of a breakup of the molecule into at least three pieces is sufficient to gather the information on the spatial orientation of the molecule, which is needed for evaluating the photoelectron interference pattern. Dictated by conservation of linear momentum, the momentum vectors of three molecular fragments lie
within a plane. They can be employed to form a coordinate frame \((x',y',z')\), which is attached to the molecular structure, as depicted in Fig. 1A. The distinct spatial orientation of the molecule within this fragment coordinate frame remains, however, unknown. In larger systems, the fragments’ emission directions are typically only loosely connected to the direction of the molecular bonds prior to the fragmentation, in particular if only few fragments are generated. Thus, the fragment frame \((x',y',z')\) deduced from the ion direction measurement and a desired spatial coordinate frame \((X,Y,Z)\) linked to distinct structural features of the molecule are typically skewed by some unknown angles \(R_X, R_Y\) and \(R_Z\), the rotation angles with respect to the \(X\), \(Y\), and \(Z\) axes). In addition, the measured ion momentum vectors alone do not provide any information on the handedness of the ionized molecule, as they define a plane and thus leave the sign of the \(Z\)-axis open, as depicted in Figs. 1B and C. Both, this information and the information on the skew-angles are, however, encoded in the electron diffraction pattern.

To extract the information from the experimental data we use the procedure outlined in Fig. 2. We start with an initial guess for the molecular structure and compute the photoelectron interference pattern in the molecular frame \((X,Y,Z)\). Then, we compare this pattern to the pattern obtained in our experiment which is provided in the fragment frame \((x',y',z')\). To quantify the agreement, we introduce the distance parameter \(d_2\) between the renormalized experimental and computed interference pattern, which also depends on the relative rotation between \((x',y',z')\) and \((X,Y,Z)\), quantified, as mentioned above, by the rotation angles \(R_X, R_Y\) and \(R_Z\) and the guess of the handedness.

\[
 d_2 = \left( \iint (I_{Exp}^{Norm}(\varphi, \cos(\Theta)) - I_{Comp}^{Norm}(\varphi, \cos(\Theta), R_X, R_Y, R_Z))^2 d\varphi d\cos \Theta \right)^{\frac{1}{2}}
\]

We now determine the skew between the coordinate frames \((x',y',z')\) and \((X,Y,Z)\) varying the three rotation angles in order to obtain the smallest distance parameter \(d_2\) (Fig. 2C). The
minimized value of $d_2$ (i.e. after applying the rotation) is then used to quantify the agreement between the measured and the computed interference pattern for the initially hypothesized molecular structure and handedness. This procedure is then repeated with a slightly adjusted molecular structure as an input in order to further minimize $d_2$. The model structure which provides the smallest distance parameter $d_2$ is assumed to be responsible for the measured interference pattern, yielding the molecular structure at the instant of ionization.

In order to test our approach, we employ the two enantiomers of methyloxirane as a benchmark system. We are using an oxygen $K$-shell photoelectron ($11.5 \text{ eV kinetic energy}$) for the electron diffraction and a naturally occurring Auger decay (subsequent to the O $1s$ photoionization) for the generation of two ionic and one neutral fragments. We focus our analysis on the fragmentation channel $\text{C}_3\text{H}_6\text{O} \rightarrow \text{C}_2\text{H}_3^+ + \text{CH}_2^+ + \text{OH}^0 + 2e^-$. The experimental data were recorded using a COLTRIMS reaction microscope\textsuperscript{30}, the theoretical modelling of the electron interference patterns has been performed by using the single-center method and code\textsuperscript{31,32}, similarly to our previous work on this molecule\textsuperscript{33}. As shown in Figs. 1B and 1C, the observed interference pattern is vastly different for the two enantiomers making chiral discrimination straightforward and the comparison to the modelled pattern shown in Fig. 2D provides the information on the absolute configuration. We employ now the algorithm outlined above in order to illustrate the high sensitivity of our approach also to the exact location of distinct atoms inside the molecule. As a first example, we show in Figs. 3A-3F the effect of a modification of the $\text{C} - \text{C}^* - \text{O}$ distance in the oxirane ring. The resulting variation of $d_2$ is shown in Fig. 2F and implies, that we are sensitive to a change of 5% of the geometry-optimized $\text{C} - \text{C}^* - \text{O}$ distance. Particularly challenging for other methods of structure determination is the assignment of the location of hydrogen atoms. Electron scattering is known to be sensitive also to such weak scatterers. Accordingly, in a second demonstration, we investigate the sensitivity of our
approach to a change of the $C^* - H$ bond length. The corresponding results are depicted in Fig. 3G which confirms, that within 5% discrepancy, the correct bond length between the chiral carbon atom and the adjacent proton attached to it, has been found via the smallest value of $d_2$.

Combining Coulomb explosion imaging of a large molecule with the measurement of the photoelectron diffraction pattern in the molecular frame and quantum chemical computation allows for precise structural analysis and chiral discrimination of molecules in the gas phase. Unlike established X-ray or several of the electron diffraction techniques, our approach does not require a molecular crystal. Contrary to traditional Coulomb Explosion Imaging, it is scalable, so that larger molecules can be examined, as well. The only requirement is that the molecule breaks sufficiently fast into at least three fragments (of which at least two are charged), so that the measured ion momentum vectors are linked to the molecular orientation at the time of ionization. In addition, by adjusting the photon energy, distinct atoms of the molecule can be addressed and the emission source of the probing electron wave inside the molecule can be selected. By applying pump-probe schemes, the method will allow for tracking changes in the molecular structure on a femtosecond time scale $^{34,35}$ in the future.
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Figure 1: Three-dimensional interference pattern of the scattered electron wave in the molecular frame of reference. A Spherical representation and definition of the molecular frame (X,Y,Z). For larger molecules, the fragment emission directions (i.e. their momenta after Coulomb explosion) do typically not coincide with molecular features such as bonds. As a result, the molecular orientation and coordinate frame (x’,y’,z’) defined by the fragments’ emission directions is rotated against the molecular frame (X,Y,Z). The panel depicts the methyloxirane molecule employed in our studies and the turquoise arrows show the directions of the measured momentum vectors of the fragments (CH$_2^+$, C$_2$H$_3^+$, and OH$^0$), which were used to generate the (x’,y’,z’)-coordinate system. The electron wave employed for probing the molecular structure has been emitted from the oxygen 1s orbital. The surrounding colored sphere shows the resulting three-dimensional probability distribution of the emission direction of the 11.5 eV photoelectron. The emission distributions are averaged over all incident directions of the ionizing light. B Same data as in A in a color-map representation. C is as B for the R-enantiomer. The mirror symmetry regarding the enantiomers is highlighted by the horizontal line to guide the eye at $\cos \theta = 0$ in B and C. A visualization of the two enantiomers and their orientation in the molecular frame are given above B and C.
Figure 2: Sketch of the optimization procedure for obtaining the molecular structure from the measured electron interference patterns. Starting with an initial guess (A) the interference pattern of the photoelectron in a chosen molecular frame (X,Y,Z) is computed (B). This computed pattern is then compared to the measured interference pattern in the fragment frame. Typically, the fragment-frame and molecular frame do not coincide. The skew between the two systems (given by the three rotation angles $R_X$, $R_Y$ and $R_Z$) is determined by finding the minimum value of distance parameter $d_2$ for the computed molecular structure (C). D shows the computed interference pattern from B in the fragment frame ($x',y',z'$). After the rotation, the minimized value of $d_2$ is used to quantify the agreement between measured and computed interference pattern for a specific hypothesized molecular structure. The molecular structure is slightly modified and the interference pattern is recomputed (E). The molecular structure at the instant of ionization is obtained for the best agreement between measured and computed interference patterns, i.e. for lowest $d_2$. 


Figure 3: Determination of the molecular structure via the best agreement between measured and computed interference pattern of the photoelectron. A–E Interference patterns from a scan in which the $CC^*-O$ distance in the oxirane ring is set to 95, 100, 105, 110 and 120 % of the optimized structure. Our structure retrieval algorithm leads within 5 % accuracy to the energy-optimized structure highlighted in green (F). G A corresponding scan of the $C^*-H$ bond length demonstrates the sensitivity of the interference pattern to weak scatterers such as hydrogen. The smallest distance in $d_2$ leads, again, within 5 % accuracy to the bond length of the energy-optimized structure.
Experimental method

The experimental data were recorded at the same beam time as the data from a previous publication. Accordingly, the identical experimental setup was used. The photon energy of 550 eV addressed the O 1s photoionization leading to a photoelectron energy of about 11.5 eV. Only electrons with kinetic energy of 11.5 ± 1.5 eV where considered in the analysis. For the data shown, the recorded data subsets with the fragmentation channels $\text{C}_3\text{H}_6\text{O} \rightarrow \text{C}_2\text{H}_3^+ + \text{CH}_2^+ + \text{OH}^0 + 2e^-$ and $\text{C}_3\text{H}_6\text{O} \rightarrow \text{C}_2\text{H}_2^+ + \text{CH}_3^+ + \text{H}_2\text{O}^0 + 2e^-$ were combined. In the molecular system, $\vec{p}_{\text{C}_2\text{H}_3^+}$ and $\vec{p}_{\text{CH}_2^+}$ points in the direction of the Y-axis and $\vec{p}_{\text{C}_2\text{H}_2^+} \times \vec{p}_{\text{CH}_3^+}$ in the direction of the Z-axis. The molecular frames defined by the fragments in the two fragmentation channels are only a few degrees twisted with respect to each other. About $3 \cdot 10^6$ events were recorded for both enantiomers and light helicities. Two other breakup channels ($\text{C}_3\text{H}_6\text{O} \rightarrow \text{C}_2\text{H}_3^+ + \text{CH}_3^+ + \text{O}^0 + 2e^-$ and $\text{C}_3\text{H}_6\text{O} \rightarrow \text{C}_2\text{H}_2^+ + \text{CH}_3^+ + \text{OH}^0 + 2e^-$) provide results similar to those shown in this paper. It turns out that for the latter fragmentation channel the CH$_3^+$ group stems from the methyl group of methyloxirane. This different fragmentation dynamics manifests itself in the fact that the measured momenta of the ions define a completely different molecular system. In addition, the interference patterns for these fragmentation channels are washed out. We suspect that this is due to a weaker correlation between measured ionic momenta and the molecular orientation at the instance of ionization due to complex fragmentation dynamics.

To calculate the distance parameter $d_2$, the minimum value in the interference pattern was first subtracted, then the integral interference pattern was normalized to one. For each calculated molecular structure, the molecular system in coordinate space used in the calculation must be connected to the measured fragment momentum vectors. To do this, we rotate the measured and calculated interference pattern with respect to each other, applying the X-Y-Z convention (roll, pitch and yaw angle: $R_X$, $R_Y$ and $R_Z$). We determine the transformation that connects the molecular system defined by the measured ionic momenta and the positions used in the computation by searching for the minimum in $d_2$ in a scan over the yaw, pitch and roll angles (Fig. 2). We scan all angles in steps of one degree. This step size is small enough to ensure that the residual error in the molecular frame does not influence the result presented in Fig. 3. The experimental statistical error is smaller than the plotted dot size; however,
different sources of systematic errors might alter the exact value of $d_2$. These sources range from limitations in the experimental angular resolution or background from other fragmentation channels to a complex interplay between areas of reduced detection efficiency on the electron and ion detectors. An estimate of our resolution when determining the three-dimensional position of the atoms is provided by considering how close the minimum in $d_2$ comes to the result of the geometry-optimized structure when scanning across different molecular structures. Thus, the resolution is estimated to range in the same size as our chosen step size of $\sim 6 \cdot 10^{-12}$ m.

**Estimate on the information content of the interference pattern**

In our present experiment, the information content is mainly limited by the statistical errors. The maximum granularity, i.e. the maximum number of discrete areas into which the interference pattern in Fig. 1 can be divided such that the statistical error is smaller than the measured change in this area. The interference patterns in Fig. 1 can be divided in 679 such areas. This number is to be compared by the degrees of freedom in the molecule, which is three times the number of atoms reduced by three translational degrees of freedom. The three degrees of freedom covering the rotation of the molecule are used to connect the fragment and molecular frame yielding $30 - 3 = 27$ degrees of freedom. This means that on average, each molecular coordinate can be resolved into about $679/27 \approx 25$ steps. However, since neither the change in the interference pattern is linearly related to the change in the molecular coordinates, nor does each molecular coordinate change the interference pattern to the same extent, no statement can be made on the relationship between the resolution in the determination of individual molecular coordinate and the information content in the interference pattern as defined above.

**Theoretical method**

The averaging of the molecular frame photoelectron angular emission distributions over all incident directions of the ionizing light was performed analytically. The average differential cross section reads:
\[
\frac{d\sigma(\theta, \varphi)}{d\Omega} = \sum_{LM} B_{LM} Y_{LM}^*(\theta, \varphi) \quad \text{with} \quad B_{LM} = \frac{1}{3} \sum_{\ell} \sum_{m'} \sum_{k} i^{\ell + \ell'} (-1)^{\ell + m'} \times \\
\times \sqrt{\frac{(2\ell + 1)(2\ell' + 1)(2L + 1)}{4\pi}} \begin{pmatrix} \ell & 0 & 0 \\ 0 & \ell' & L \\ 0 & -m' & M \end{pmatrix} A_{\ell m k} A_{\ell' m' k}. 
\]

Here, \( \theta \) and \( \varphi \) are the photoelectron emission angles in the frame of molecular reference, \( Y_{LM} \) are the spherical functions, and \( A_{\ell m k} \) are the dipole transition amplitudes for the emission of the partial photoelectron waves with the angular momentum quantum numbers \( \ell \) and \( m \) via the absorption of a photon of polarization \( k \), as defined in the frame of the molecule. Because of the mutual orthogonality of the Wigner rotational matrices (which transform the ionizing light of a given polarization from the laboratory to the molecular frame), the average molecular frame photoelectron angular distribution is independent of the polarization of the ionizing light that is used in the experiment. The ionization transition amplitudes \( A_{\ell m k} \) for the emission of O(1s) photoelectrons of the methyloxirane enantiomers were computed by the single-center method and code\textsuperscript{31,32} in the relaxed-core Hartree-Fock approximation, as described in our previous work on this molecule\textsuperscript{33} (see the supplementary information document of this reference for more details).

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**Competing interests:** The authors declare that they have no competing interests.

**Data and materials availability:** All data needed to evaluate the conclusions in the paper are present in the paper. Additional data related to this paper may be requested from the authors. Correspondence and requests for materials should be addressed to K.F. (fehre@atom.uni-frankfurt.de), P.V.D. (demekhin@physik.uni-kassel.de), or M.S.S. (schoeffler@atom.uni-frankfurt.de).