

MS12-05 | ALEPH: A NEW SOFTWARE FOR STRUCTURAL ANALYSIS AND GENERATION OF FRAGMENT LIBRARIES FOR MOLECULAR REPLACEMENT

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RCIMBOLDO [1] is a fragment based molecular replacement framework where Local Folds (LF: small discontinuous fragments) are located with PHASER [2] providing phases that are improved and interpreted in SHELXE [3].

ALEPH [4] is a program for retrieving structural properties of proteins from the PDB [5], based solely on geometrical descriptors, Characteristic Vectors (CVs) [6], computed as centroid C α -O vectors on consecutive tripeptides. Networks of CVs hold angles and distances representing protein structure.

ALEPH implements four different tasks:

- Annotation: a customizable secondary and tertiary structure analysis to map general or local properties controlling the strictness of the annotation.
- Decomposition: structure subdivision into smaller compact folds. ARCIMBOLDO_SHREDDER [1] gives the model internal degrees of freedom based on this decomposition.
- Library generation: to extract and cluster fragment libraries collecting structural variations of the same fold. Each library expresses a common pattern as the hypothesis for phasing whereas ARCIMBOLDO_BORGES [1] jointly evaluates results for all models, revealing correct solutions.
- Superposition: align a fragment onto a complete structure.
- A graphical user interface is provided to perform each task and to visualize and plot the results in real time.

[1] Millán, C. *et al.*, (2015) IUCrJ., 1, 95.

[2] McCoy, AJ, *et al.* (2007). J Appl Crystallogr 40, 658.

[3] Usón, I & Sheldrick, G. (2018) Acta Cryst. D74, 106.

[4] Medina, A., *et al.* (2019) In preparation.

[5] Berman, H., *et al.* (2015) Nucleic Acids Research. 35, D301

[6] Sammito, M., *et al.* (2013). Nat Methods. 10, 1099.