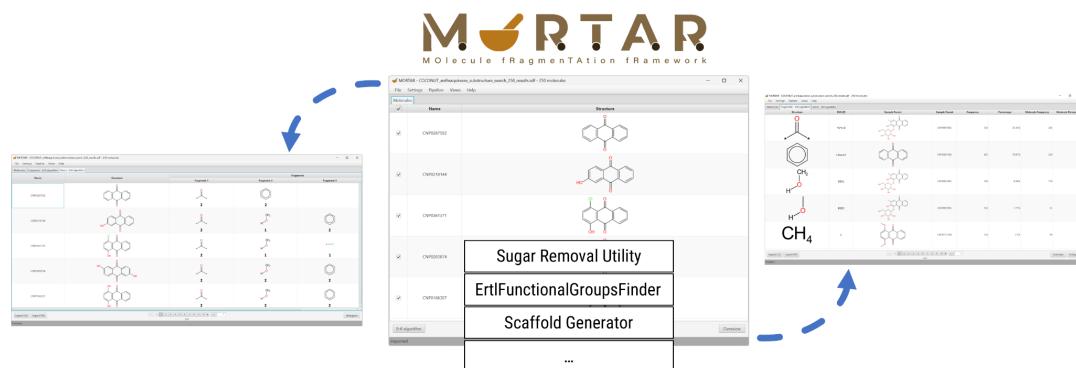


MORTAR – A Rich Client Application for *in silico* Molecule Fragmentation

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The process of developing and implementing computational algorithms to extract specific substructures from molecular graphs, known as *in silico* molecular fragmentation, is a repetitive task that involves multiple iterations of applying a set of rules to relevant structural data, followed by checking and adjusting the results. This requires a computational workflow that includes data import, fragmentation algorithm integration, and result visualization. When developing a new algorithm, this workflow is not readily available and must be built from scratch.



To address this problem, this work presents MORTAR (MOlecle fRagmenTAtion fRamework) [1], an open Java-based graphical user interface application that supports the development of new *in silico* molecule fragmentation algorithms as well as their availability after publication. The MORTAR application provides various visualization options for the fragmentation results of a group of molecules and basic analysis functions. Fragmentation algorithms can be integrated and developed within MORTAR using a special wrapper class. In addition, any combination of the available fragmentation methods can be used to run fragmentation pipelines. Currently, three fragmentation methods are integrated in MORTAR: ErtlFunctionalGroupsFinder [2], Sugar Removal Utility [3], and Scaffold Generator [4]. All cheminformatics functionality within MORTAR is implemented using the Chemistry Development Kit (CDK).

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