# Design in 2D, model in 3D: Live 3D pose generation from 2D sketches

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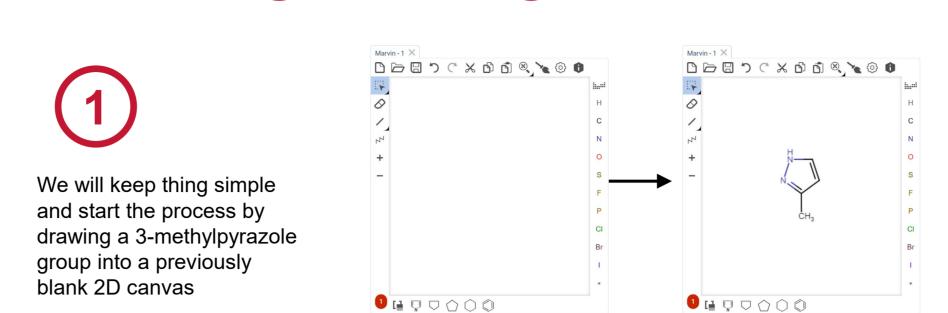
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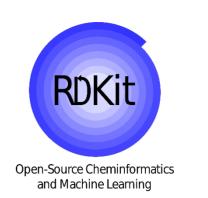


### Idea

The main idea which sparked the *grow3D* project was: how nice would it be to draw a molecule in your favorite 2D sketcher and simply see it grow sensibly within the binding site in the 3D viewport, naturally obeying to the constraints imposed by the active site, with little or no intervention from the user?

## Flow diagram for grow3D



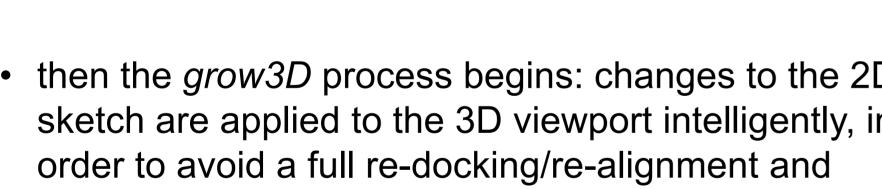


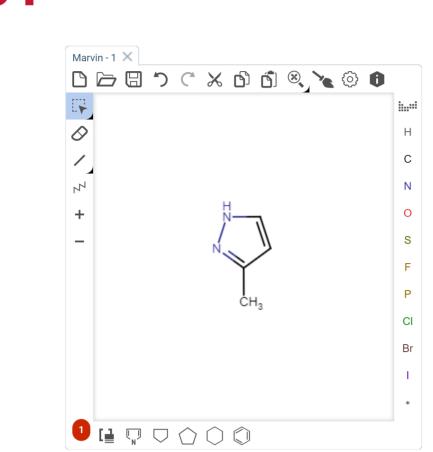
The RDKit is extensively used throughout the *grow3d* workflow for substructure matching, MCS finding, file parsing, etc.

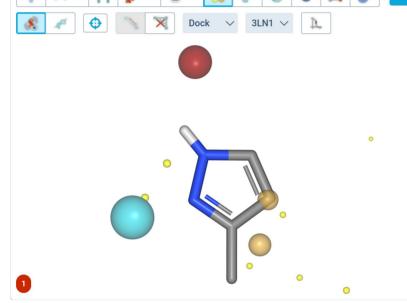
### How hard can it be?

In a nutshell:

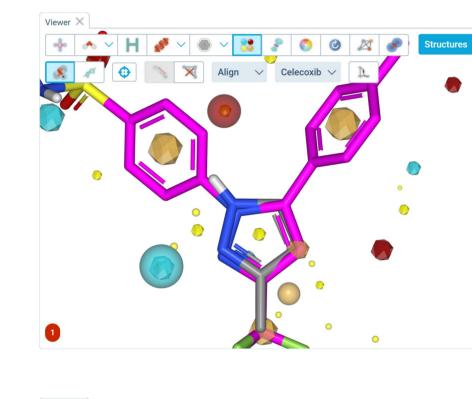
- You sketch some starter structure in the 2D editor (or upload it from your hard drive, or copy/paste it from any source, such as your ELN)
- The largest 2D fragment is popped to a 3D conformation...
- ... and docked into the protein's active site
- ...or 3D field/shape aligned against a reference...
- ...using the protein as excluded volume (if available)









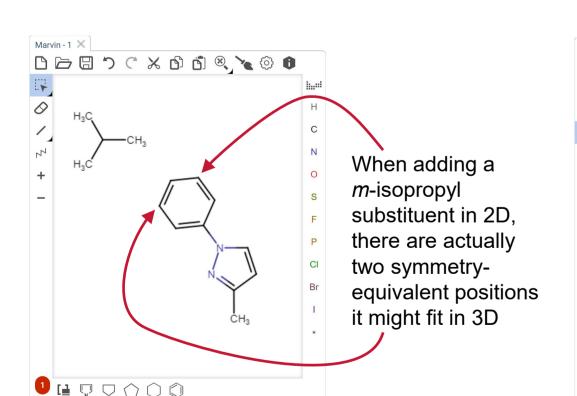


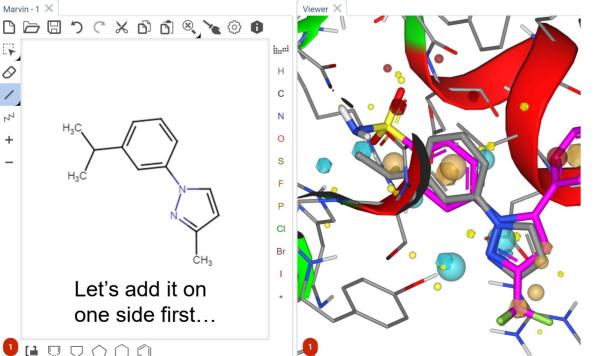


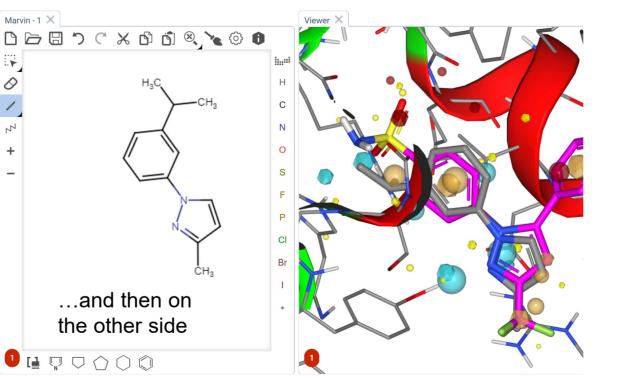
• then the *grow3D* process begins: changes to the 2D sketch are applied to the 3D viewport intelligently, in allow real-time 3D feedback on the 2D design.

#### Has the Dock into Has the Look at disconnected YES YES Generate 3D number of binding site (A) total number number of 2D fragments which structure for the 2D frags or align to of atoms frags changed? make up the sketch new 2D frag increased? increased' reference (B) No fragments → N/ NO NO Bonds/atoms Frags were Let's add combined or deleted were deleted a methyl group in position ' on the pyrazole Map current 2D frags to previous 2D frags Atoms were deleted Compare Loop over 2D Pair current # indices of frags: does this frag 2D indices current frag Check: frag have 3D to previous with previous coords? • Element Bonds Formal A methyl group was added No action • Find bonds to Generate 3D added atoms Align to reference coords for newly Delete those (C) and wait for added 2D frag bonds and cap the next edit with hydrogens Attach to parent Align frag Hs with Let's turn with appropriate parent's heavy atoms the 1-methyl bond order and vice versa substituent into a 1-benzyl substituent A phenyl ring was added Align to reference (D) and wait for score and do a local optimization the next edit • Find bonds to added atoms Spin around bond Delete those and score against bonds and cap reference with hydrogens Generate 3D Align frag Hs with Attach to parent parent's heavy atoms coords for newly with appropriate added 2D frag bond order and vice versa

## The devil is in the details (1): Symmetries





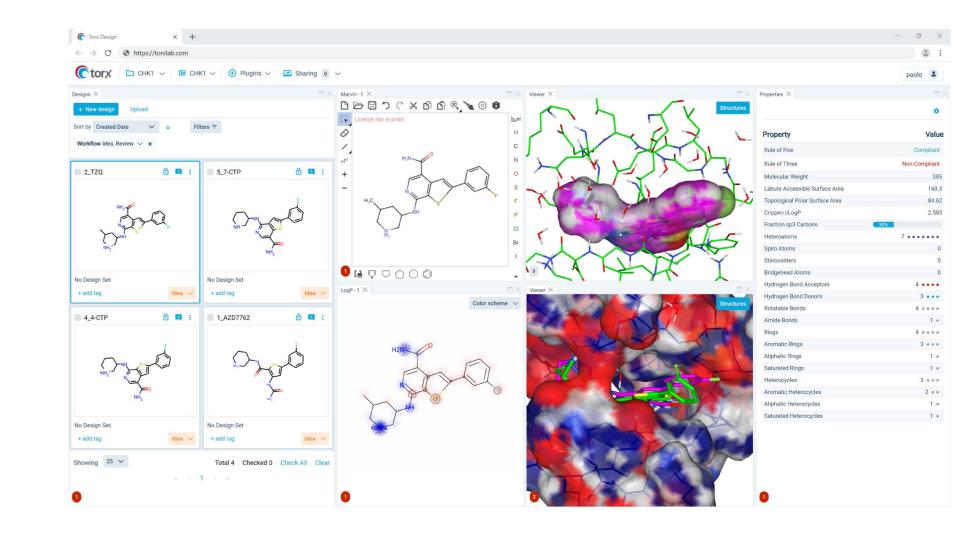


which side the isopropyl substituent is drawn in 2D, the grow3D algorithm chooses the one which fits the active site

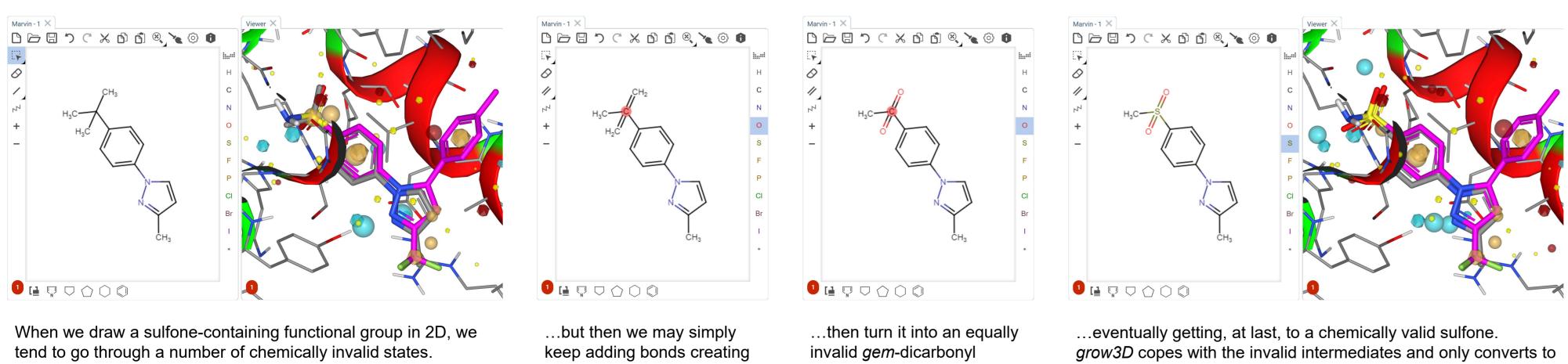
No matter

### Conclusions

- grow3D is an algorithm which generates sensible 3D poses in response to edits to a 2D sketch
- Poses are scored against their ability to fit a binding site and/or mimic electrostatics and shape of a reference ligand
- The algorithm is enough quick and accurate to enable real time assessment of design ideas
- grow3D is part of Torx<sup>™</sup>,<sup>1</sup> the new web-based Cresset platform for collaborative small molecule discovery chemistry



# The devil is in the details (2): Chemically invalid states



beast...

tend to go through a number of chemically invalid states. We keep adding methyl groups until we get to a *t*-butyl, which is chemically valid...

- a chemically invalid gem-bismethylidene intermediate...
- - 3D the chemically valid molecules.

# References and Acknowledgements

- 1. www.torx-software.com
- 2. Thank you to ChemAxon for the provision of Marvin JS<sup>©</sup>